GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

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Title:
Perfect score:
Sequence:
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Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0 seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTMAVLRNRKGGKGPLRRRP...
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1780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A_Geneseq_101002: *
                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseq
                                                                                                                                                                                                                                                                                                                                                                                                                                           'SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl
                                                          SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.
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                                                                            !/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Search time 38 Seconds (without alignments)
1202.762 Million cell updates/sec
                                                                                                                                                                                                                     /geneseqp-emb1/AA1991
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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305	707	504	402	396	324	298	289	228	289	338	150	301	339	272	329	323	310	310	237	252	237	237	237	237	237	146	76	130	175	258	255	255	197	190
22	2	21	21	21	21	21	2	22	20	22	23	22	22	22	22	23	22	22	22	23	23	22	22	22	20	22	21	22	21	21	23	22	22	22
AAM93493	AAR60110	AAG39296	AAG39297	AAG39298 .	AAG13409	AAG13410	AAG13411	ABB60184	AAY59954	ABB65069	ABG60220	ABB65078	AAE10329	AAM25877	AAM39908	ABB06073	AAB94285	AAM94003	AAM93832	ABP51311	ABP51811	AAB95201	AAM93682	AAU27754	AAY34129	ABB12265	AAG03290	AAM25242	AAB53339	AAB41622	ABP51810	AAE04891	AAG73901	ABG16368
 Human polypeptide,	1		thal	thal	Arabidopsis thalia		-	Drosophila melanog	Human endometrium	Drosophila melanog	Human DITHP polype	Drosophila melanog	Human transporter	Human protein segu	_	NS prote	-	Human stomach canc				Human protein sequ		_	_	_	Ξ.	_	-	ORFX ORF138	_	transp	n colon	Novel human diagno

ALIGNMENTS

RESULT 1 AAB15537

AAB15537 standard; Protein; 271 A A

AAB15537;

28-FEB-2001 (first entry)

Human immune system molecule from Incyte clone 2751129.

immunosuppressive; cytostatic; fungicide; protozoacide; ant: gene therapy; diagnostic; immunological disorder; viral info bacterial infection; fungal infection; parasitic infection; antiarteriosclerotic; antiasthmatic; antidiabetic; nephrotropi antigout; dermatological; antithyroid; virucide; hepatotropic; Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianaemic; antiarteriosclerotic; antiasthmatic; antidiabetic; nephrotropic; cano antibacterial; infection; immunogen. antibody;

Homo sapiens.

WO200060080-A2.

12-OCT-2000

04-APR-2000; 2000WO-US09072.

05-APR-1999; 05-MAY-1999; 99US-0127852. 99US-0132647.

(INCY-) INCYTE PHARM INC

Yue H, Lal P, Tang YT, Baughn MR, Azimzai Y, Lu DAM;

WPI; 2000-665005/64.

N-PSDB; AAA95776

Claim 1; Page

77;

95pp; English

New human immune system molecules 1-15 and polynucleotides encoding them useful for diagnosing, treating or preventing e.g. immunologic disorders, infections, cell proliferative disorders, microbial

reventing e.g. immunological disorders, microbial

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RESULT 2
ABB28752
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Best Local Sim
Matches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders (e.g. actinic keratosis, arteriosclerosis, bursitis), and cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also useful as immunogens for the development of antibodies that specifically recognizes these peptides. The polynucleotides may be used to detect and quantify gene expression in blopsied tissues in which expression of IMOL may be correlated with the disease, as targets in a microarray, to detect differences in gene sequences among normal, carrier and affected individuals, and for secreening libraries of compounds in drug screening techniques. Antibodies which specifically bind to IMOL may be used for the diagnosis of disorders characterized by expression of IMOL, or in assays to monitor patients being treated with IMOL or agonists, antagonists, or inhibitors of IMOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           may be used to treat or prevent disorders associated with decreased expression or activity of IMOL, such as immunological disorders (e.g. inflammation, actinic keratosis, AIDS, Addison's disease), haematopoietic cancer, infections caused by virus (e.g. adenovirus, parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococc Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g. Shigella), fungi (e.g. Aspergillus, Blastomyces), cell proliferative disorders (e.g. actinic keratosis, arteriosclerosis, bursitis), and changes (e.g. actinic keratosis, arteriosclerosis, bursitis), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis, treatment or prevention of immunological disorders, infections and cell proliferative disorders, including cancer. The IMOL may be used to treat or prevent disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a human immune
                Homo sapiens
                                                                                                                                                          01-FEB-2002
                                                                                                                                                                                                  ABB28752
                                                         disease; cancer
                                                                            Human; microarray; single exon probe; gene expression;
                                                                                                              Peptide #1403 encoded by breast cell single exon nucleic acid probe
                                                                                                                                                                                                                                      ABB28752 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA95775-A95789),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVVVTGREPDSRRQDGAMSSSDAEDDFLEPATFTATQAGHALPLLPQEFPEVVPLNIGGA
                                                                                                                                                                                                                                                                                                                                          GRPALPSSRSVSSRRRCPSPPMSVRSSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HFTTRLSTLRCYEDTMLAAMFSGRHY I PTDSEGRYFIDRDGTHFGDVLNFLRSGDLPPRE
                                                                                                                                                                                                                                                                                                                                                                                QRKA----RFAKLKSLTPSWLMSVLIKMP
                                                                                                                                                                                                                                                                                                                                                                                                                        RVRAVYKEAQYYAIGPLLEQLENMQPLKGEKVRQAFLGLMPYYKDHLERIVEIAGCVRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVRAVYKEAQYYAIGPLLEQLENMQPLKGEKVRQAFLGLMPYYKDHLERIVEIAR-LRAV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDVLNFLRSGDLPPRE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA isolated
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                                                                                                                                                                                                                                      Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and compositions comprising them are useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51,4%;
                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as clone
                                                                                                                                                                                                                                        56
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Pred. No. 3.3e-74;
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                                                                                                                                                                                                                                                                                                                                                                                299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 271;
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RESULT 3
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a spatially-addressable set of single exonucleic acid probes for measuring sene expression in a sample deriving mean breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mana of human breast, and then measuring the label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New spatially-addressable set of single exon nucleic acid probes useful for measuring gene expression in sample derived from huma breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 11720; 327pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-496933/54.
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                                                                                                           Human; foetal liver; gene expression; single exon nucleic acid
                                                                                                                                                           Peptide #1445 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                             04-FEB-2002
                                                                                                                                                                                                                                                          АВВ33939
                                                                                                                                                                                                                                                                                                       ABB33939 standard; Peptide; 56 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bound to each probe of the microarray. The probes are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 FPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF 199
                                                                                                                                                                                                                                                                                                                                                                                                                             1 FPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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2000US-0207456
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                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.1%; Score 305; DB 22; 100.0%; Pred. No. 3.7e-20;
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Best Local S
Matches 56
              04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       measuring and
fetal liver. T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                           Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                          Protein #1374 encoded by probe
                                                                                                                                                                                                                                                                                                                                         23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid measuring human gene expression in a sample derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
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                                                                                                                         30-JAN-2001; 2001WO-US00666
                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                   WO200157274-A2
                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                              congenital
                                                                                                                                                                                                                                                                                                                                                                                                      ABB19375 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liver. The single exon nucleic acid probes may be used for predicting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 AA;
                                                          2000US-0180312.
2000US-0207456.
2000US-0608408.
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2000US-0236359
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                                             2000US-0632366
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
3.7e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probe for from human foetal
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RESULT 5
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Best Local
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26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; brain expressed exon; gen
microarray; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in hearts -
                                             WPI; 2001-483446/52
                                                                                                   Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epilepsy; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e. The probes may be used for predicting, measuring and displaying expression in samples derived from the human heart via microarrays.
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                                                                                             Hanzel DK,
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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Single exon nucleic acid probes

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                                                  probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
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Sequence
                                                                                                                                                                                                             The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                            Example
                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow -
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27-SEP-2000;
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30-JUN-2000;
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microarray; cancer; leukaemia; lymphoma; myeloma.
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   56
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2000US-0207456.
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
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Pred. No.
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3.7e-20;
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Query Match

17.18;

Score 305;

B 22;

Length 56;

RESULT 8
AAM27397

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RESULT 7
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                                                                   Query Match
Best Local Similarity
                                                       Matches
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                          (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                  WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cervical cancer
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                                                                                                             Sequence
                                                                                                                                                    Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                 The present invention relates to human single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                       analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                 cervical cancer.
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                           144 FPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF
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FPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF
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                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                                                                                                                                      genome-derived
                                                        56;
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                                                                                                                                                                                                                                                                                                             SEQ ID No 19789; 487pp; English.
                                                                                                                                                                                                                                                                                                                                         gene
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                                                                                                             56 AA;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                       Conservative
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                         expression
                                                                    17.18;
                                                                                                                                                                                                                                                                                                                                                    single exon
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                                                                   Score 305;
Pred. No.
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; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                             Rank
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                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                    nucleic
                                                                                                                                                                                                                                                                                                                                       cervical ep
                                                                                                                                                                                                                                                                                                                                                                                                             DR;
                                                     ; DB 22;
. 3.7e-20;
ches 0;
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                                                                                                                                                                                                                                                                                                                                       epithelial cells -
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                                                                                Length
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56
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RESULT 9
AAM02689
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Best Local 9
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26-MAY-2000;
30-JUN-2000;
                                                                  Probe; human; inflammatory d
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes (SENP: see ANI3315-ANI57546). The present sequence is a peptide encoded by on such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
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                                                                                                      Peptide #1371 encoded by probe for measuring breast gene expression
                                                                                                                                       09-OCT-2001
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               WO200157270-A2
                                         Homo sapiens
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27-SEP-2000;
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                                                                                                                                                                                                                                                                           144 FPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF 199
                                                                                                                                                                                                                                                                                                                     Local Similarity tes '56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID No 27666; 654pp;
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                                                                                                                                                                                                                                                                                                                                                                              56 AA;
                                                                                                                                                                                                                                                                                                                    17.1%; Scilarity 100.0%; F
Conservative 0;
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                   disease;
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                                                                                  disease;
                                                                  proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56
                                                                                                                                                                                                                                                                                                                                    Score 305;
Pred. No.
                                                                                  breast cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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                                                                   breast
                                                                                                                                                                                                                                                                                                                     ; DB 22;
. 3.7e-20;
ches 0;
                                                                   disease;
                                                                                 development disorder;
                                                                                                                                                                                                                                                                                                                                              Length 56;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                   non-carcinoma tumour
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ABG36762
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Query Match
Best Local Similarity
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03-AUG-2000;
21-SEP-2000;
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26-MAY-2000;
                          WO200186003-A2
                                                                               primary ciliary
hyaline membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel single exon
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04-OCT-2000;
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                                                    Homo sapiens.
                                                                                                                                                                                                                      Human peptide
                                                                                                                                                                                                                                                   19-AUG-2002
                                                                                                                                                                                                                                                                              ABG36762
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                                                                                  membrane
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15-NOV-2001

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Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel single exon nucleic acid probes (see AAI0010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting diagnosing the human breast.
                  Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndr
pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
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                                                                                                                                                                                                                                                                 ABG36762 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                      144 FPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID No 11429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                           17.1%;
larity 100.0%;
Conservative (
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2000US-0207456
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                                                                                                                                                                                             (first entry)
                                                                                                                                                        encoded by genome-derived single exon
dyskinesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid probe used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322pp;
                                                                                                                                                                                                                                                                   56
                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                fibrocystic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 56;
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                                                                                                                                                          probe SEQ
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              dysplasia;
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                                  syndrome;
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y from WIPO
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                                                                                                                                                                                                                                                                                                                                                         56
                                                                                                                                                          26427.
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30-JAN-2001;

2001WO-US00665

20000S-180312P

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CC probes: Also included are a microarray comprising the novel set of cc probes. Also included are a microarray comprising the novel set of cc nucleic acid expressed in the human lung; measuring gene expression in a cc sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with cc array; identifying exons in a eukaryotic genome, comprising cc of the eukaryotic; and (b) detecting specific hybridisation of detectably clabeled nucleic acids from eukaryote lung mRNA, to a single exon probe of the eukaryotic; and (b) detecting specific hybridisation of detectably cc labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, comprising (a) identifying exons from genomic sequence by the method cc in the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method cc above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon from common pattern of cc expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the cc probes/open reading frames (ORF). The probes are used for gene cc expression analysis, and for identifying exons in a gene, particularly using human lung disease (ILD), familial idiopathic pulmonary disease. CC comprision, neurofibromatosis, tuberous sclerosis, gaucher's disease, lungary disease, lungary disease, lemmansky-pudlak syndrome, sarcoidostis, pulmonary
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                                                                                         Query Match
Best Local S
Matches 56
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                   pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The resent sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spatially-addressable set of single exon nucleic acid probes, used measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn
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21-SEP-2000;
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
                                                                                                                                                                                                                                                  of the printed specification, format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                            naemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complements or the 12387 open reading frames derived from the
                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2614 nucleic acid
56; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                   56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probes for measuring gene expression in a sample ung comprising single exon nucleic acid probes hav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000GB-0024263.
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2000US-236359P.
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2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nprising single exon nucleic acid probes having one sequences mentioned in the specification, or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                         Score 305; DB 23;
Pred. No. 3.7e-20;
0; Mismatches 0;
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                                                                                                                                    Length 56
                                                                                           Indels
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RESULT 11
ABG16368
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                       , Q
                                                                              Matches
                                                                                              Query Match
Best Local
                                                                                                                                                                                                                  diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                         for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639362/73.
N-PSDB; AAS80555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG16368 standard; Protein; 190
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID No 46727; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #16359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                     87 PGAARRARGMVVVTGREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPE 146
ហ
                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
PGALPLAQVICMWQGCAVE--RPVGSMTSQTPLPQSPRPRRPTMS
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                                                                                                   Similarity
                                                                                                                                                              190
                                                                                Conservative
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                                                                                                                                                              Ä
                                                                                                 15.8%;
                                                                           ; Score 282; DB 22;
; Pred. No. 2.7e-17;
34; Mismatches 66
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                                                                                66;
                                                                                                                 Length 190;
                                                                              Indels
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147 VVPLNIGGAHETTRLSTLRCYEDTMLAAMESCRHYIPTDSEGRYFIDRDGTHFGDVLNFL 206

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ID AAG
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                                                                                                                                                                    the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletion. In a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of patients.
                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-235357/24.
N-PSDB; AAH33332.
                             present invention.

N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                          inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into sost cell and culturing the cell by inserting the proteins. N and P can be used in the prevention, diagnos and treatment of colorectal carcinomas and cancers. AAH37196 to AAH3720 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                              AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), wher
                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 6463-6464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colorectal carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG73901;
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 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVELNVGGEFHTTTLGTLRKFPGSKLAEMFSSLAKASTDAEGRFFIDRPSTYFRPILDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTGQV-PTQHIPEVYREAQFYEIKPLVKLLEDMPQIFGEQVSRKQFLLQVPGYSENLELM 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSGDLPPRERVRAVYKEAQYYAIGPLLEQLENMQPLKGEKV-RQAFLGLMPYYKDHLERI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colon cancer; colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barash SC,
 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer antigen
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99US-0163280.
Å
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein SEQ ID
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                                                                                                                                                                                                                                                                                                                                                               English.
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                                                sequences
                                                                 sequence listing were
                                              are present
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                                                                                                               diagnosis
AAH37204
                                                                                                                                                                                                               deletions
                                                 for
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Query Match Best Local S Matches 66

Similarity

15.6%;

Score 278; DB 23 Pred. No. 6.5e-17 Mismatches

22; 57;

Length 197; Indels

16;

Gaps

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The present sequence is transporter and ion channel-4 (TRICH-4) protein. TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth disease, Duchenne muscular dystrophy, angina and hypertension,

Claim

1.

English

Conservative

29;

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RESULT 13
AAE044991
AXX AAE04
XXX AAE04
XXX AAE04
XXX AAE04
XX AAE04
XXX AAE04
XXX Huma
XXX Huma
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28-JAN-2000;
02-FEB-2000;
10-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophyperrension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzhaimer's disease; pellepsy; mood; arrhythmia; pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stro) Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy; demyelinating disease; mental disorder; Schizophrenia; polymyositis; muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease; dermatomyositis; diabetes mellitus; immunological disorder; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human transporter and ion channel-4 (TRICH-4) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE04891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE04891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1999;
14-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-SEP-2001
                                                                                                                                                                                                                                                           Novel human transporter and ion channel and preventing transport, neurological,
                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baughn MR,
Hillman JL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         malabsorption syndrome; hypercholesterolaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus;
sickle cell anaemia; Wilson's disease; infertility; Cushing's disease;
scleroderma; pulmonary artery stenosis; nootropic; Addison's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-DEC-2000; 2000WO-US35095
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                                                                                                                                                                                                                                                                                                                                             AAD09555
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                                                                                                                                                                                  Page 116-117; 160pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Burford N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000US-0177332.
; 2000US-0178572.
; 2000US-0179758.
; 2000US-0181625.
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Nguyen
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DB,
                                                                                                                                                                                                                                                           proteins useful for treating muscle and immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                              Yang J,
Yao MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Reddy
Gandhi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder, dementia, depression, epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, pick's disease, Huntington's disease, and parkinson's disease, demyelinating diseases, mental disorders including mood, anxiety, Schizophrenia and seasonal affective disorder, muscle disorder including cardiomyopathy, myocarditis, polymyositis, dermatomyositis, arrhythmias and asthma and immunological disorders including AIDS, adult respiratory distress syndrome (ARDS), allergies, anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythematosus and other diseases including sickle cell anaemia, Milson's disease, cataracts, infertility, pulmonary artery stenosis, Grave's disease, Cushing's disease, Addison's disease, cushing's disease, Addison's disease, paoriasis and viral, bacterial, fungal, helminthic and protozoal infections. TRICH DNA is useful in gene therapy and in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local :
                                                  Feder JN,
Chang H;
WPI; 2002-583519/62
                                                                                                                                                                                                                                                                                                                                                                                WO200248369-A2
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                                                                                                                                                                                     02-NOV-2000;
21-DEC-2000;
                                                                                                                                                                                                                                                                      01-NOV-2001; 2001WO-US50726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense therapy; neuronal growth; neuronal damage; neuronal disorder; neurodegenerative condition; autoimmune disease; inflammatory condition; hyperproliferative disease; cancer; cardiovascular disorder; infection; cerebrovascular disease; inflammation; vaccine; lymphatic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human potassium channel beta-subunit K+Mbetal protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP51810 standard; Protein; 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            purposes.
                                                                                                                                                                                                                                                                                                                        20-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    angiogenesis;
                                                                                                                             (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antimigraine; cytostatic; vulnerary; antibacterial; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppressive; nephrotropic; neuroprotective; antiinflammatory;
antithyroid; dermatological; cardiant; vasotropic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; potassium channel beta-subunit; K+Mbetal; potassium channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological disorders including Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 EIKPLVKLLEDMPQIFGEQVSRKQFLLQVPGYSENLELMVKLARAEAI 161
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                                                                           Lee LM,
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                                                                                                                                                                                     2000US-245366P.
2000US-257851P.
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39.3%;
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Pred. No. 9.4e-17;
                                                                           Jackson D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                                                           Ramanathan C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255;
                                                                           Siemers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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Novel human potassium channel beta-subunit, K+MBETAl polypeptide and polynucleotides for diagnosing, prognosing, preventing, treating immune, hyperproliferative, cardiovascular disorder and for identifying
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PHYX

N-PSDB; ABQ73684

Claim 33; Fig 1A-B; 316pp; English

35555555555555555555555553838

CC can be used for screening candidate compounds (small molecules) capable co f binding to and/or modulating activity of a potassium channel beta-cc subunit, by contacting a test compound with a substantially or partially cc purified (I) and selecting as candidate compounds those test compounds that bind to and/or modulate activity of the polypeptide. (I) stimulates cc neuronal growth which can be used to treat, prevent, and/or diagnose cc neuronal damage which occurs in certain neuronal disorders or neuro-cc degenerative conditions. (I) can be used in treating, preventing and/or diagnosing diseases, disorders or conditions associated with: autoimmune cdiseases; inflammatory conditions; hyperproliferative diseases; cancer; cc diagnosing diseases, disorders or conditions associated with: autoimmune cdiseases; inflammation; and cc diseases; inflammation; and cc diseases; inflammation; and cc diseases; inflammation; and cc dadywant that enhances immune responses to an antigen, as a adjuvant to enhance tumour-specific immune responses. Further (I) is useful as a stimulator of B cell responsiveness to pathogens, as an activator of T cells, as an agint to boost immunoresponsiveness among aged populations and conditions and conditions as a stimulator of a stimulator of a stimulator of suseful as a stimulator as a stimulator of suseful as a stimulator of suseful as a stimulator of a stimulator of a stimulator of suseful as a stim K+Mbetal (I). (I) has immunosuppressive, nephrotropic, neartithyroid, dermatological, antiinflammatory, cardiant, and/or neonates, as a stimulator of cytokines, to enhance or inhibit complement mediated cell lysis, for stimulating wound and tissue repair, anglogenesis, and the repair of vascular or lymphatic diseases or anticoagulant, antimigraine, The present sequence represents the human potassium activities, and can be used in gene therapy and antisense therapy. (I) has immunosuppressive, nephrotropic, neuroprotective, cytostatic, vulnerary and antibacterial channel beta subunit vasotropic,

Sequence 255 8

Ş, Query Match Best Local Matches RODGAMSSSDAEDDFLEPATFTATQAGHALFILFQEFFEVVFLNIGGAHFTTRLSTLRCY 167 al Similarity 66; Conserv Conservative 15.6%; 29; Score 278; DB 23; Pred. No. 9.4e-17; 29; Mismatches 57 57; Length 255; Indels 16; Gaps ω,

B 9 RPVGRMTSQTPLPQSPRPRRPTMS--------TVVELNVGGEFHTTTLGTLRKF 54

밁 S 168 55 PGSKLAEMFSSLAKASTDAEGRFFIDRPSTYFRPILDYLRTGQV-PTQHIPEVYREAQFY EDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDVLNFLRSGDLPPRERVRAVYKEAQYY 227

114 EIKPLVKLLEDMPQIFGEQVSRKQFLLQVPGYSENLELMVRLARAEAI 161 AIGPLLEQUENMQPLKGEKY-RQAFLGLMPYYKDHLERIVEIARLRAV 274

S

RESULT 15 AAB41622

AAB41622 standard; Protein; 258

AAB41622;

08-FEB-2001 (first entry)

Human ORFX ORF1386 polypeptide sequence SEQ ID NO:2772.

antianaemic; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory, antiviral; antibacterial; antifungal; antirheumatic; antithyroid vulnerary; antipsoriatic; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; gene therapy; cancer; proliferative disorder; immunosuppressant; nootropic; neuroprotective; immunosuppressant; cardiant; ; hypertension; disease;

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immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiafammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating the predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating the presence of or predisposition and preventing or treating the proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, or preventing or preventing the proteins and preventing disease, diabetes mellitus, the preventing of the proteins of the prevention of the proteins of the prevention of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
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02-APR-1999; 99US-0127636,
05-APR-1999; 99US-0127728,
30-MAR-2000; 2000US-0540763
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N-PSDB; AAC75831.
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Query Match Best Local Similarity

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228 AIGPLLEQLENMQPLKGEKY-RQAFLGLMPYYKDHLERIVEIARLRAV 274 | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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Search completed: February 12, 2003, 11:07:32 Job time: 39 secs

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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen
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US-09-142-791A-6
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US-08-470-339-189
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US-08-470-339-189
US-08-459-558-170
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Sequence 12. Appl
Sequence 14. Appl
Sequence 14. Appl
Sequence 27. Appl
Sequence 10. Appl
Sequence 2. Appli
Sequence 4. Appli
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Sequence 4. Appli
Sequence 5. Appli
Sequence 5. Appli
Sequence 6. Appli
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Sequence
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Sequence
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            170, App

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170, App

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170, App
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GENERAL INCOMPATION:

APPLICANT: Miller, Andrew P.

APPLICANT: Curran, Mark Edward

APPLICANT: Hu, Ping

APPLICANT: Wang, Jian-Wang

FILE REFERENCE: SEQ-15P

CURRENT APPLICATION NUMBER: US/09/336,643A

CURRENT FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 60/076,687

PRIOR APPLICATION NUMBER: 60/076,448

PRIOR FILING DATE: 1999-01-19

PRIOR PRILING DATE: 1999-01-19

PRIOR APPLICATION NUMBER: PCT/US99/03826

PRIOR FILING DATE: 1999-02-22

NUMBER OF SEQ ID NOS: 87

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 25

LENGTH: 237

TYPE: PRT

ORGANISM: H. sapiens

US-09-336-643A-25
RESULT 2
US-09-336-643A-12
; Sequence 12, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
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US-09-336-643A-25
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Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                             148 VPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIDTDSEGRYFIDRDGTHFGDVLNFLR 207
                                                                                                                                                                                 120
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                                                                                                                                                                                                                             265 IVEIARLRAVOR 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVELSSTRKLSK 131
                                                                                                                                                                                                                                                                          TSELTLPLDFKEFDLLRKEADFYQIEPLIQCLNDPKPL--
                                                                                                                                                                                                                                                                                                                    SGDLP---PRERVRAVYKEAQYYAIGPLLEQLENMOPLKGEKVRQAFLGLMPYYKDHLER 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25, Application US/09336643A
o. 6399761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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US-08-341-018-72
US-08-3470-335-170
US-08-735-021-170
US-08-735-021-170
US-08-467-602-170
US-08-467-602-170
US-08-467-602-324
PCT-US94-05083C-186
PCT-US94-05083C-186
PCT-US95-06846A-170
US-08-467-602-326
US-08-467-602-328
US-08-467-602-328
US-08-467-602-335-246
US-08-467-602-336
US-08-467-602-336
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Pred. No. 3.8
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Result No.

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; LENGTH: 812
; TYPE: PRT
; ORGANISM: Homo saplens
US-09-166-350-12
                                                                                                                                                  Query Match
Best Local Similarity 33.9
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 258
TYPE: PRT
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           MARLIER APPLICATION NUMBER: US 09/166,350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: Scanlan, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: Chen, Yao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLICANT: Stockert, Elisabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207
                                                                                                                         134 GH--ALPLLPQEFPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYF 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 VVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDVLNFL 206
                                       192 IDRDGTHFGDVLNFLRSGDLPPR-ERVRAVYKEAQYYAIGPLLEQLENMQPLKGEKVRQA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 9.6%;
Local Similarity 38.9%;
hes 37; Conservative 7
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LICANT: Knuth, Alex
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  64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE: L0461/705
                                                                                 4 GHCGSFPAAAAGSGEIVQLNVGGTRFSTSRQTLMWIPDSFFSSLLSGRISTLRDETGAIF 63
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FILING DATE: 1999-02-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSGDLPPRERVR----AVYKEAQYYAIGPLLEQLEN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMTLNVGGYLYITQKQTLTKYPDTFLEGIVNGKILCPFDADGHYFIDRDGLLFRHVLNFL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/166,350A
FILING DATE: 1998-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/336,643A FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INVENTION: No. 6399761el Human Potassium Channels
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Curran, Mark Edward
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WFLRTKELDLRGVSINVLRHEAEFYGITPLVRRLLLCEELERSSCGSV 123
                                                                                                                                                                                       33.9%;
                                                                                                                                                                                       9.3%; Score 165; DB 4; Length 812
33.9%; Pred. No. 1.1e-07;
                                                                                                                                                               20; Mismatches
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Pred. No. 5.3e-09;
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: LOCATION: (1)...(256)
: OTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-643A-14
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT ELIING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: CT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                               APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: NO. 6399761el Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
                                                                                                                                                                                                                                                                                                                                                                                                                 atent No.
                                                                                                                                   PRIOR APPLICATION NUMBER: 60/076,687 PRIOR FILING DATE: 1998-08-07
                                                                                                                                                                                   CURRENT
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ORGANISM: H. sapiens
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                                                                                                              PRIOR APPLICATION NUMBER: 60/116,448
                                                                                                                                                                                                                                                                                                                                                               PPLICANT: Miller, Andrew P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 PATPTATQAGHALPLLPQEFPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 -FLGLMP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 DS-EGRYFIDRDGTHFGDVLNFLRSGDLPPRERVR---AVYKEAQYYAIGPLLEQLE 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 PASPLXNQ-GIPTPAQLTKSNAPVHIDVGGHWYTSSLATLTKYPESRIGRLFDGTEPIVL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 DSLKQHYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPMLLEME 125
                                           FILING DATE: 1999-01-19
APPLICATION NUMBER: PCT/US99/03826
FILING DATE: 1999-02-22
                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                   FILING DATE: 1999-06-3
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INVENTION: No. 6399761el Human Potassium Channels
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                                                                                                                                                                                                                                                                                                                                          Curran, Mark Edward
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Windows Version 4.0
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Pred. No. 1e-07;
25; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 256;
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SEQ ID NO 27 LENGTH: 389

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; ORGANISM: H. :
US-09-336-643A-27
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                                            Query Match
Best Local Similarity
Watches 41; Conserv
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Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: L1, M1
                                                                                                                                                                                                             TELEX: 25-3533
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: L1, Min
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tent No.
                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171
                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108
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                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                     NAME: Kilyk Jr., John REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDDDVLFVCEGE-PFIDPQTDSKPPEG-----LLGFHTDWLTLNVGGRYFTTTRSTLVNK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGINLLGVLE 170
EVLVVNVSGRRFETWKNTLDRYPDTLLGS--SEKEFFYDAESGEYFFDRDPDMFRHVLNF 59
                          EVVPLNIGGAHETTRLSTLRCYEDTMLAAMESGRHYIPTDSEGRYFIDRDGTHFGDVLNF 205
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                                                                                                                                                                                  amino acid
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Two Prudential Plaza, Suite
                                                                                                                                                                                               162 amino acids
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                                                          Conservative
                                                                                                                                                    linear
                                                                                                                                   protein
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                                                                                                                                                                 single
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32.3%;
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Pred. No. 5e-07;
                                                                        Score 138; DB 2;
Pred. No. 4.6e-06;
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                                                          Mismatches
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Sequence 2, Application US/09142791A Patent No. 6368823

GENERAL INFORMATION:

APPLICANT: Antoine Michel Alain Bril
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-François Simon Pierre Faivre
APPLICANT: Jean-Luc Javre

APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012

APPLICATION NUMBER: US/09/142,791A FILING DATE: 1999-02-02

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RESULT 8
US-09-142-791A-2
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/336,643A
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                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)...(646)
OTHER INFORMATION: Xa
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: H. sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: Wang, Jian-Wang
ITLE OF INVENTION: No. 6399761el Human Potassium
ILE REFERENCE: SEQ-15P
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                                                                         138
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                                                                                                                                                                 186 SEGRYFIDRDGTHFGDVLNFLRSGDL---PPRERVRAVYKEAQYYAIGPLLEQ----LENMQ 240
                                                                                                                                                                                                                                                  137 LPLLPQEFP------EVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTD 185
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                                                                                                        241 PLKGEKVRQAFLGLMPYYKDHLERIVE 267
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                                                                                                                                                                                                           LPPAQQPLPPAPGVKASRGDXVLVVNVSGRRFETWKNTLDRYPDTLLGS--SEKEFFYDA 77
                                                                       DRK-----KENAERLAE 149
                                                                                                                                           DSGEYFFDRDPDMFRHVLNFYRTGRLHCPRQECIQAFDEELAFYGLVPELVGDCCLEEYR
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                                                                                                                                                                                                                                                                                                    Score 133.5; DB Pred. No. 0.00011
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                                                                                                                                                                                                                                                                                                                    Length 646;
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PRIOR APPLICATION NUMBER: PCT/EP98/01901 PRIOR FILING DATE: 1998-03-23

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; ORGANISM: human
US-09-178-109-4
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                                                                                                                                                        RESULT 10
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SEQ ID NO 4
LENGTH: 636
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                                                                            GENERAL INFORMATION:
                                                                                               Sequence 4, Application US/09142791A Patent No. 6368823
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Best Local Similarity
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            APPLICANT: Antoine Michel Alain Bril
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-François Simon Pierre Falvre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Human Potassium Channel Polynucleotides and TITLE OF INVENTION: Polypeptides and Uses Therefor FILE REFERENCE: ahp-98089
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APPLICANT: Diks, Daniel W.
APPLICANT: Chang Ling, Huai-Ping
APPLICANT: Sokol, Patricia T.
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                                                                                                                                                                                                                                                                                               27 MPLAPADKNKRQDELIVLNYSGRRFQTWRTTLERYPDTLLGS--TEKEFFFNEDTKEYFF 84
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APPLICATION NUMBER: EP 97403007.4
FILING DATE: 1997-12-11
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                                                                                                                                                                                                                  DRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGILP 125
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LING DATE: 1997-03-27
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Jean-Luc Javre
                                                                                                                                                                                                                                                                                                                                                                           7.1%; Score 127; DB 4; ilarity 34.7%; Pred. No. 0.00047; Conservative 15; Mismatches 43
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LENGTH: 655
TYPE: PRT
ORGANISM: human
US-09-178-109-2
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US-09-178-109-2
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US-09-142-791A-4
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Best Local :
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                                                                                                                                                                         Query Match
Best Local Similarity
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SOFTWARE: FastSEQ for Windows
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                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEC
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                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Human Potassium Channel Polynucleotides and TITLE OF INVENTION: Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dilks, Daniel W.
APPLICANT: Chang Ling, Huai-Ping
APPLICANT: Sokol, Patricia T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/EP98/01901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: ahp-9808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TILE REFERENCE: GH-30012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                              137 LPLLP----QEFPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFI| 192
                                                                                                                                                                                                                                                                                                                ID NO 2
                                      193 DRDGTHFGDVLNFLRSGDL--PPRERVRAVYKEAQYYAIGP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 DRDGTHFGDVLNFLRSGDL--PPRERVRAVYKEAQYYAIGP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 LPLLP----QEEPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFI 192
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  85
                                                                          27 MPLAPADKNKRODELIVLNVSGRRFQTWRTTLERYPDTLLGS--TEKEFFFNEDTKEYFF 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 DRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGILP 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: EP 97403007.4
DRDPEVFRCVLNEYRTGKLHYPRYECISAYDDELAFYGILP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MPLAPADKNKRODELIVLNVSGRRFOTWRTTLERYPDTLLGS--TEKEFFFNEDTKEYFF
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Similarity 34.78;
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                                                                                                                                                                   7.1%; Score 127; DB 4;
34.7%; Pred. No. 0.00049;
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Pred. No. 0.00049;
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                                                                                                                                                   Gaps
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RESUL7 12 US-09-142-791A-6 ; Sequence 6, Application US/09142791A ; Patent No. 6368823

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US-08-606-143-45
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; ORGANISM: HOMO SAPIENS
US-09-142-791A-6
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Best Local Similarity 27.08;
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LENGTH: 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/EP98/01901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION: NOVEL COMPOUNDS ILE REFERENCE: GH-30012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ent No.
                                                       ATTORNEY/AGENT INFORMATION: NAME: Kilyk Jr., John
                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 LPLLP----QEFPEVVPLNIGGAHFTTRLSTLRCYEDIMLAAMFSGRHYIPTDSEGRYFI 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 DRDGTHFGDVLNFLRSGDLPPRERVRAVYKEAQYYAIGPLLEQLENMQPLKGEKVRQAFL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE OF INVENTION:
                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 60601
                                                                                           APPLICATION NUMBER: FILING DATE: 23-FEICLASSIFICATION: 51
                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
RRENT APPLICATION DATA:
aborTreamon unmapp. HG/N8/606 143
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        REGISTRATIÓN NUMBER: 307
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                   TITY: Chicago
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AGENT INFO-
Kilyk Jr., John
Kilyk Jr., 30763
NUMBER: 30763
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Thierry Paul Gerard Calmels
Jean-François Simon Pierre Faivre
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Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOUNDS AND RELATED METHODS FOR MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH COMPOUNDS
                                                                                                                                     US/08/606,143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 42;
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	TVPSWPTAPVPSAGEPGEEAPYL-VKV 164	106 GEAGAWGGDREPPAAGPRALGPPAEEPLLAANGTVPSWPTAPVPSAGEPGEEAPYL-VKV		밁	
	PATPTATQAGHALPLLPQEF 144	115SSDAEDDFLE		γQ	
	RKAAAAA	59ASVCYSSPPSVGSVQELAQRAA		Дb	
	SMVVVTGREPDSRRQDGAMS 114	62 EGATALPPAHCLSPPSGQPAAGRVMPGAARRARGMVVVTGREPDSRRQDGAMS		Qy	
	LPALRIGELPANQGGTSAASASSGRRSGQAPAGRERVGV 61	9 RKGGKGPLRRRPLALPALRLGELPAN(40	
14;	DB 4; Length 349; 13; 98; Indels 97; Gaps	Match 6.1%; Score 108.5; Local Similarity 23.5%; Pred. No. 0.0 tocal Similarity 23.5%; Mismatches 70; Conservative 33; Mismatches	Query M Best Lo Matches		
		PR PR	6	us;	
		EARLIER APPLICATION NUMBER: 08/036,555 EARLIER FILING DATE: 1993-03-24 NUMBER OF SEQ ID NOS: 252 SOSTWARE: FastSEQ for Windows Version 4.0	EARLIER EARLIER NUMBER SOFTWAR		
	5.F.	LE OF INVENTION: PREPARATION AND USE REFERENCE: 04585/00200B RENT APPLICATION NUMBER: US/08/470,335F RENT FILING DATE: 1995-06-06	TITLE OF FILE RECURRENT CURRENT		
	DRS, THEIR	CANT: CHEN, MARIO S. CANT: HILES, IAN OF INVENTION: GLIAL MITOGENIC	APPLI	~ ~ ~	
	· · · · · · · · · · · · · · · · · · ·	STROOBANT, F MINGHETTI, I WATERFIELD, MARCHIONNI,	APPLI APPLI	. ~. ~. ~.	
		NO. 6147190 INFORMATION: ANT: GOODEARL, ANDREW	Patent GENERAL APPLIC		
		14 470-335-188 ence 188, Application US/08470335F	Seque	RE US	
		258 YKDHLERIVEIA 269 : : : 97 YKDRRRENAERLQDDA 112		da Vo	
	OPLKGEKVROAFLGLMDy 257	207 RSGDLPPRERVRAVYKEAQYYAIGPLLEQLENMQPLKGEKVRQAFLGLMP		Qy Db	
	SGRHYIPTDSEGRYFIDRDGTHFGDVLNEL 206	147 VVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIDTDSEGRYFIDRDGTHFGDVLNEL		Qy Db	
4;	.5; DB 2; Length 159; 0.00031; hes 44; Indels 39; Gaps	Match 6.7%; Score 119.5; Local Similarity 28.7%; Pred. No. 0.0 0.0 39; Conservative 14; Mismatches	Query M Best Lo Matches		
		TELEFAX: (312) 616-5700 TELEX: 25-533 INFORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS: LENGTH: 159 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein 08-606-143-45	INFOR	g	
		TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 616-5600	IBT IBT	·· ··	

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Search completed: February 12, 2003, 11:09:23
Job time : 18 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 23:
Matches 70; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 382
LENGTH: 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND TLE OF INVENTION: DISORDERS LE REFERENCE: 04585/028003
                                                                                                                                                                                                                                                                                                                                                     115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 DANSTSRAPAAFRA-SFPPLETGRNLKKEVSRVLCKRCALPPRLKEMKSQESAAGSKL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 DGTHFGDVLNFLRSGDLPPRERVRAVYKE-----AQYYAIGPLLEQLENMQPLKGEKV 247
                                                                                                                                                                                                                                                  145 PEVVPLNIGG----AHFTTRLSTLRCYEDTMLAAMFSGRHYIPT-----DSEGRYFIDR 194
                                                                                                                                                                                                                                                                                                    140 GEAGAWGGDREPPAAGPRALGPPAEEPLLAANGTVPSWPTAPVPSAGEPGEEAPYL-VKV 198
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                                                                                                   246 DANSTSRAPAAFRA-SFPPLETGRNLKKEVSRVLCKRCALPPRLKEMKSQESAAGSKL 302
                                                                                                                                               195 DGTHFGDVLNFLRSGDLPPRERVRAVYKE-----AQYYAIGPLLEQLENMQPLKGEKV 247
                                                                                                                                                                                                   199 HQVWAVKAGGLKKDSLLTVRLGTW-
                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                              62 EGATALPPAHCLSPPSGQPAAGRYMPGAARRARGMYYYTGREPDSRRQDGAMS----- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 RSGRPGPRAQRPGSAARSSPPLPLLPLLLLL----GTAALAPGAAAGNEAAPAG------ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 RKGGKGPLRRRPLA------LPALRLGELPANQGGTSAASASSGRRSGQAPAGRERVGV 61
                                                                                                                                                                                                                                                                                                                                                                                                    -----ASVCYSSP---PSVGSVQELAQRAA---VVIEGKVHPQRRQQGALDRKAAAAA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/467,602C
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Gwynne, David I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.1%; Score 108.5; DB 4; 23.5%; Pred. No. 0.015; ative 33; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                     ---SSDAEDDFLE-----PATPTAT-----QAGHALPLLPQEF 144
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                                                                                                                                                                                                   -GHPAFPSCGRLKEDSRYIFFMEP 245
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Score
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Gapop 10.0 ,
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1780
1 MTMAVLRNRKGGKGPLRRRP...
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CIKS_RABIT
CIKS_BROME
MYCN_HUMAN
5ES_RAT
CIKZ_HUMAN
5ES_RAT
CIKZ_HUMAN
CIKB_DROME
CIKZ_HUMAN
NUCG_MOUSE
CIKZ_MOUSE
CIKZ_MOUSE
GAG_SMRVH
FGDI_MOUSE
CIK3_HUMAN
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Y176_HUMAN
MYCN_MARMO
CIK5_MUSPF
MN1_HUMAN
CIK1_MOUSE
CIK1_MOUSE
CIK1_RAT
TCOF_HUMAN
CIK1_HUMAN
FG21_HUMAN
FG21_HUMAN
CIK2_XENLA
SM6C_RAT
ROXN_HUMAN
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Compugen Ltd
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InterPro; IPR00310; BTB_POZ.
InterPro; IPR003131; K_tetra.
InterPro; IPR0214; K_tetra; 1.
SMART; SM00225; BTB; 1.
PROSITE; PS50097; BTB; 1.
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	rough a the EMBI restric restric tent is y and i ,.isb-sil	LIPOPOLYS	W., Lee K.L	Katz R.W., Shows T. factor-alpha-induced	<pre>Euteleostom1; ; Homo.</pre>	endothelial (P17658 P40330 Q01956 P10180 O35762 Q9wv48 P78426 O75949 Q28527 P13808 P30305 P30305 P26762
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MEDLINE=96281124; PubMed=8724849;

MEDLINE=96281124; PubMed=8724849;

Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;

Prediction of the coding sequences of unidentified human

The coding sequences of 40 new genes (KIAA0161-KIAA0200) d

analysis of cDNA clones from human cell line KG-1.";

DNA Res. 3:17-24 (20196).

DNA Res. 3:17-24 (20196).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                           SEQUENCE
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InterPro: IPR003131; K_tetra.
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                                                             LRLGELPANQGGTSAASASSGRRSGQAPAGRERVGVEGATALPPAHCLSP-PSGQPAAGR
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1; SM00225; BTB; 1.
[TE; PS50097; BTB;
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                                     LQLDPAMAGLGG----
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25.0%;
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Pred. No. 0.0005;
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Q61976;
15-DEC-1998
15-DEC-1998
15-DEC-1998
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EMBL; X53674; CAA37712.1;
HSSP; P25912; 1HLO.
                            SEQUENCE
                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Fourel G., Tiollais P., Buendia M.-A.;
"Nucleotide sequence of the woodchuck N-myc gene (WN-mycl).";
Nucleic Acids Res. 18:4918-4918(1990).

-i- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
BHLH PROTEIN. BINDS DNA AS AN HEFERODIKER WITH MAX.

-i- SIMILARITY: BELLONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
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                                                     MOD_RES
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                                                                                                                                                            PROSITE; PS00038; HLH_1; 1. PROSITE; PS50888; HLH_2; 1.
                                                                                                                                                                                        SMART; SM00353;
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Pfam; PF01056; Myc_N_term; 1.
PRINTS; PR00044; LEUZIPPRMYC.
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  Score 123;
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PHOSPHORYLATION (BY CK2)
(BY SIMILARITY).
                                                                                                       ASP/GLU-RICH (ACIDIC).

BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                        (BY
                                                   PHOSPHORYLATION (BY CK2)
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ASP/GLU-RICH (ACIDIC).
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Sciurognathi; Sciuridae;
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                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mustela putorius furo (Ferret)
                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Heart atrium;
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9669;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein.
DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO
                                                                                                                                                    EVERY THIRD POSITION.

DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
                                                                                                                                        CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GREPD-----SRRQDGAMSSSDAEDDFLEP------ATPTATQAGHALPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELAHPAAECVDPAVVFPFPVNKRDPAPVPVAPAGSPAVGAAVAGAAAPASAAVAAPPRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VR--PKNAALGLGRAQ-SSELILKRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRPANGGDHKALSTSGEDTLSDSDDEEDDEEEDEEEEIDVVTVEKRRSSSNSKAVTTFTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVLRNRKGGKGPLRRRPLALPALRLGELPANQGGTSAASASSGRRSGQAPAGRERVGVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QRRNDLRSSFLTL----RDHVPELVK-----NEKAAKVVILKKAT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----YVESEDAPPQKKIKSEVSPRPLKSVIP--PKAKSLSPRNSDSEDSERRRNHNILER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVLNFLRSGDLPPRERVRAVYKEAQYYAIGPLLEQLENMQPLKGEK--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQEFPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVSEKLQHGRGP----PAAGPA-----TPGAGAANPAGRGHGGTAGAGRAGAALPA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VRQAFLGLMPYYKDHLERIVEIARLRAVQRKARFAKLKSLT
U45979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 39, Created)
(Rel. 39, Last sequence up
(Rel. 39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         potassium
AAB41145.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.09
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fissipedia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 0.097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rtebrata; Euteleostomi;
Mustelidae; Mustelinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -VPIHQQHNYAAPSP----
                                                                                                                                        SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mustelinae;
                                                                                                                                                                                                                                                      AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114;
                                                                                                                                                                                                                                         ACIDS
                                                                                                                                                                                                                                                       SI
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  15 FFF F F F R 200000
                                                                                                                                     CIKL_DROME
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0169; KCHANNEL
PRINTS; PRO1512; KY15CHANNEL
PRINTS; PRO1491; KYCHANNEL
PRINTS; PRO1496; SHAKERCHAN
SMART; SM00225; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                               Voltage-gated potassium channel protein Shal SHAL OR SHAL2 OR CG9262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00520; lon_trans; Pfam; PF02214; K_tetra; 1.
brosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Man
Insecta; Pterygota; Neoptera; Endop
Muscomorpha; Ephydroidea; Drosophil
NCBI_TaxID=7227;
                                                                           P17971; 09VW11;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; Q54397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                           CIKL_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              onic channel;
                                                                                                                                                                                                                                                     242
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                                                                                                                                                                                  264
                                                                                                                                                                                                         301
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                                                                                                                                                                                                                                                                            156
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                                                                                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .ycoprotein;
                                                                                                                                                                                                                                                                                                                                                                    52 -----RARG----TQRGVD----PGGRPLPPLPQDPQQPRRLPPEDEEGEGDPALGMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                      26 LRLGELPANQGGTSAASASSGRRSGQAPAGRERVGVEGATALPPAHCLSPPSGQPAAGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                 MEIALVPLENGG-----AMTVRGGGEAGTGCSQ-AIGGELQCPPTAGLSDGPKEPAP--+
                                                                                                                                                                                                                                                                                                                                                                                         MPGAARRARGMVVVTGREPDSRRQDGAMSSSDAEDDFLEP-ATPTATQAGHALPLLPQEF
                                                                                                                                                                                                         GVTSWINAERRLYLETPI ----
                                                                                                                                                                                                                                                     L-KGEKVRQAFLGLMPYYKDHLERIVETARLRAVQRKARFAKLKSLTPSWLMSVLIKMPP
                                                                                                                                                                                                                                                                                                                       DQVLGAGSLHHQRVLINISGLRFETQLGTLAQFPNTLLGDPAKRLRYFDPLRNE--YFFP
                                                                                                                                                                                                                                                                                                                                             PEV-----VPLNIGGAHFTTRLSTLRCYEDTMLAAMFSG-RHYIPTDSEGRYFID
                                                                                                                                                                                                                               LPRNEFQROVWL
                                                                                                                                                                                                                                                                           RNRPSFDGILYYYQSGGRLRRPVNVSLDVFADEIRFYQLGDEAMERFREDEGFIKEEEKP
                                                                                                                                                                                                                                                                                                RDGTHFGDVLNFLRSGD---LPPRERVRAVYKEAQYYAIG-PLLEQL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                              81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                  -FRDERELLRHPPVPHQPLGPSRGAN-GSGPLAPPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KV15CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHAKERCHANEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334
366
407
443
504
          Arthropoda; Mandibulata;
Neoptera; Endopterygota;
oidea; Drosophilidae; Dros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K_channel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEGMENT S1.
SEGMENT S2.
SEGMENT S3.
SEGMENT S5.
SEGMENT S6.
SEGMENT S6.
POLY-GIY.
N-1-TWEET.
                                                                                                                                                                                                      GPERQNNEKKSPVQLPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 122.5; D
Pred. No. 0.15;
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N-LINKED (GLCNAC...
                                                                                                                                                                                                                               IFEYPESSGSARGIAIVSVLVILISIITFCLETLPE
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                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142DB9F8CBB43FE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transport; Voltage-gated
                                                                                        update)
                                                                                                                           490
         ata; Pancrustacea;
ota; Diptera; Brack
Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             148;
                                                                  (Shal2).
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                                                                                                                                                                                                        336
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL
                       Brachycera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601;
                                                                                                                                                                                                                                                                                                --ENMQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                channel;
                                  Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                               193
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                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                      300
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A Harris N.L. Harvey D. Heiman T.J., Wei M.-H., Ibegwam C.,

A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Retchum K.J.

A Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Melson D.R., Melson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Weiskas R., Tector C., Furner R., Venter E., Wang A.H., Wang X.,

RA Weiskas R., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.

RT "The genome sequence of Drosophila melanogaster.";

"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wei A., Covari
"Shal, Shab, a
Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Devies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Devies P., Debablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.
                                                                                                                                                                                                                                                                                                                                                                                                                      Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M.D., Celniker S.E., Holt R. Amanatides P.G., Scherer S.E., Li
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SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006;
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                                                                                                                                                                                                           FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES, ASSUMING OPENED OR CLOSED COMPORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERNCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT, MAY PLAY A ROLE IN THE NERVOUS SYSTEM AND IN THE REGULATION OF BEATING FREQUENCY IN PACEMAKER CELLS.
SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
                                                               SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
PRODUCED BY ALTERNATIVE SPLICING.
DOMAIN: THE ANINO TERMINUS MAY BE IMPORTANT IN DETERMINING RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CIN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE C
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       CHARACTERIZED
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                                                SUBCELLULAR COMPARTMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed-10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Butler A., Baker K., Pak M., Salkoff L.; three genes encoding potassium channels in
                         SEGMENT S4
     SERIES
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IS PROBABLY THE VOLTAGE-SENSOR AND OF POSITIVELY CHARGED AMINO ACIDS A
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                                                                  I MAY PLAY A ROLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang X.,
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Б.,
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Matches 41
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InterPro; IPR003091;
InterPro; IPR003131;
InterPro; IPR003968;
InterPro; IPR000636;
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TRANSMEM
CARBOHYD
CARBOHYD
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Q61762;
                                                                          MOUSE
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         KCNA5
                 Voltage-gated
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PRINTS; PRO1497; SHAI
SMART; SMO0225; BTB;
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SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene model prediction.
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86 204
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                 potassium
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                                                                STANDARD;
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353
408
55918
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41,
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406
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27.0%;
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M+channel_nlg.
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K+channel_pore
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                                              Created)
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                  channel
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                                                                                                                                                                                                                        s; Score 121; DBpred. No. 0.1517; Mismatches
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SEGMENT S2.
SEGMENT S3.
SEGMENT S4.
SEGMENT S5.
SEGMENT S6.
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N-LINKED
N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                  on transport; Voltage-gated 
Alternative splicing.
                  tation update)
protein Kv1.5
                                     update)
                                                                                                                                                                                                                                                                      602
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                (KV1-5).
                                                                                                                                                                                                                                                               CRC64;
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<u>ن</u>

musculus

(Mouse)

14;

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Pfam; PR00520; ion_trans; 1.
Pfam; PF02214; K_tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01512; KV1SCHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01496; SHAKERCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L22218; AA
HSSP; Q54397; 1E
MGD; MGI:96662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-Heart;
PubMed-8226976;
Pillant P.,
Pillant P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. B101. Chem. 268:24283-24289(1993).

-I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSEI CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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                  DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
   CARBOHYD
                                           TRANSMEM
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                                                                                                                                                              lonic channel;
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DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER SIMILARITY: TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND MODERATELY IN BRAIN. LOW LEVELS IN THYMUS, SKELETAL MUSCLE AND SPLEEN. I EXPRESSED IN LIVER, LUNG OR KIDNEY.

DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND KV1-5/3'; ARE PRODUCED BY ALTERNATIVE SPLICING. NON-FUNCTIONAL BUT INHIBITS EXPRESSION OF KV1-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS: 3 ISOFORMS; KV1-5 (SHOWN HERE),
                                                                                                                                                                                                                                                                                           ; IPR004052;
; IPR003091;
; IPR003131;
; IPR003968;
; IPR000636;
                                                                                                                                                                                                                                                                            IPR003968; Kv_channel.
IPR000636; M+channel_nlg.
IPR003972; Shaker_channel.
                                                                                                                                                                                                                                                                                                                                                                   IPR001622;
                                                                                                                                                                                                                                                                                                                                                                                 IPR000210;
 AAA39365.1; -.
1BL8.
                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                          KV15channel.
                                                                                                                                                                                                                                                                                                                         K_tetra.
                                                                                                                                                                                                                                                                                                                                       K_channel.
                                                                                                                                                                                                                                                                                                                                                                   K+channel_pore.
                                                                                                                                                                                                                                                                                                                                                                                   BTB_POZ
                                                                                                                                               tamily;
                                          SEGMENT S1.
SEGMENT S2.
SEGMENT S3.
SEGMENT S4.
SEGMENT S5.
SEGMENT S6.
                                                                     SEGMENT
SEGMENT
POLY-GLY.
N-LINKED
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                                                                                                                                               Phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guillemare E.,
                                                                                                                                                           transport; Voltage-gated channel;
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THE VOLTAGE-DEPENDENT POTASSIUM
THE VOLTAGE-DEPENDENT POTASSIUM
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
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"Molecular cloning
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Homo sapiens (Human).
Homo sapiens (Human).
Homo sapiens (Human).
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         Nelson D.J., Steiner D.F.;
"Sequence and functional expression in Xenopus oocytes
insulinoma and islet potassium channel.";
proc. Natl. Acad. Sci. U.S.A. 88:53-57(1991).
                                                        TISSUE=Insulinoma;
MEDLINE=91095456;
                                                                                                             channel cDNAs from
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                                                Philipson L.H., Hice R.E.,
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ed potassium channel protein Kvl.5
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ice R.E., Schaefer
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h K.M., Walbridge
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RL Genomics 12:729-737(1992).

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTAGSIUM CO ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE COMPORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE COMPORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE COMPORMATIONS IN RESPONSE OF THE SECRETIVE CHANNEL THROUGH WHICH K + IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT. MAY PLAY A ROLE IN REGULATING THE SECRETION OF INSULIN CC. IN NORMAL PANCREATIC ISLETS.

CC IN NORMAL PANCREATIC ISLETS.

CC IN NORMAL PANCREATION: INTEGRAL CHANNEL PROTEINS (PROBABLE).

CC IN SUBCULTULAR LOCATION: INTEGRAL CHANNEL PROTEINS (PROBABLE).

CC IN SUBCULTURE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHANNEL THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHANNEL THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHANNEL THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE COMPANIN THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPANIMENTS.

CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPANIMENTS.

CC IN MODULATION OF SHAKER POTASSIUM CHANNEL SUBFAMILY.

CC IN SPECIFIC SUBCELLULAR COMPANIMENTS.
                                                                                                                                                                                                                                                       Pfam; PF00520; ion_trans; 1.
Pfam; PF02214; K_tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01512; KV15CHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01495; SHAKERCHANEL.
SMART; SM00225; BTB; 1.
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EMBL; M55513; AAA36422.1; -.
EMBL; M55524; AAA60146.1; -.
PIR; B39922; B39922.
HSSP; Q54397; 1BL8.
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                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003091; K_channel.
InterPro; IPR003131; K_tetra.
InterPro; IPR00368; Kv_channel.
InterPro; IPR000636; M+channel_nlq.
InterPro; IPR003972; Shaker_channel.
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Molecular cloning, characterization, and genomic localization of a
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Pfam; PF02214; K_tetra; 1.
PRINTS; PR00169; KCHANNEL.
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PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01491; SHAKERHANEL.
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HSSP; Q54397; 1BLB.
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SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
                                                                                      QEFPEV--
                                                                                                                                                                           MEISLVPLENG----SAMTLRGGGEAGAS---
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FPNTLLGDPAKRLHYFDPLRNE--YFFDRNRPSFDGILYYYQSGGRLRRPVNVSLDVFAD 189
                          YEDTMLAAMFSGRHYI-PTDSEGRYFIDRDGTHFGDVLNFLRSGD---LPPRERVRAVYK 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KV15CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHAKERCHANEL
                                                                                                                                                                                                                                                                                                               10
116
181
181
535
546
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M+channel_nlg.
Shaker_channel.
                                                                                                                                                                                                                                                  6.4%;
                                                                                                                                                                                                                                                                                                66552 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KV15channel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K_tetra.
                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (BY PHOSPHORYLATION))
                                                                                                                                                                                                                                  Score 113.5;
Pred. No. 0.64
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEGMENT S1.
SEGMENT S2.
SEGMENT S3.
SEGMENT S4.
SEGMENT S5.
SEGMENT S6.
                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ion transp
ly; Phosphor
SEGMENT S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transport; Voltage-gated channel; nosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                  GLCNAC...
D (GLCNAC...
D (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC
                                                                                                                                                                                                                                                  . 64 ;
                                                                                                                  B
                                                                                 ---- VPLNIGGAHFTTRLSTLRC
                                                                                                                                                                                                                                                                   B
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78)
78)
78)
78)
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PKA)
                                                                                                                  ---- ANQGGRPLPPMA
                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                           -CVQTPRGECGCPPT
                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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                                                                                                                                                                                                                                                                   602;
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                                                                                                                                                                                                                                     Gaps
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                                                       131
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                                                                                                                                            141
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         RESULT

OCCORDER REPRESENTATION

OCCORDER REPR
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QYY618; Q9Y5019; Q13354; Q00613; Q13416;
16-QCT-2001 (Rel. 40, Created)
16-QCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nuclear receptor co-repressor 2 (N-CoR2) (Silencing mediator retinoic acid and thyroid hormone receptor) (SMRT) (SMRTe) (Tretinoic acid receptor-associated co-repressor) (T3 receptor-retinoic-acid-receptor-associated co-repressor) (T3 receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _HUMAN
NCR2_HUMAN
Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S., Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A., "CDNAs with long CGA trinuclectide repeats from human brain."; Hum. Genet. 100:114-122(1997).

-1. FUNCTION: MEDIATES THE TRANSCRIPTIONAL REPRESSION ACTIVITY OF SOME NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, THUS PREVENTING ACCESS OF THE BASAL TRANSCRIPTION.

-1. SUBUNIT: FORMS A LARGE COREPRESSOR COMPLEX THAT CONTAINS SIN3A/B AND HISTONE DEACETYLASES HDAC1 AND HDAC2. THIS COMPLEX ASSOCIATES WITH THE THYROID (TR) AND THE RETINOID ACID RECEPTORS (RAR) IN THE ABSENCE OF LIGAND, AND MAY STABILIZE THEIR INTERACTION WITH TFIIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sande S., Privalsky M.L.;
"Identification of TRACs (T3 receptor-associating cofactors), a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ordentlich P., Downes M., Xie W., Genin A., Spinner N.B., Eval "Unique forms of human and mouse nuclear receptor corepressor Proc. Natl. Acad. Sci. U.S.A. 96:2639-2644(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM SMRT).
TISSUE-Pituitary;
MEDLINE-99178941; PubMed-10077563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Fetal liver;
MEDLINE-96408715; PubMed-8813722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptors.";
Nature 377:454-457(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Cervical adenocarcinoma;
MEDLINE-96008552; PubMed-756612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-9919215; PubMed-10097068;
Park E.J., Schroen D.J., Yang M., Li H., Li L., Chen J
"SMRTe, a silencing mediator for retinoid and thyroid
receptors-extended isoform that is more related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM SMRT).
TISSUE-Cervical adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             associating
                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM TRAC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A transcriptional co-repressor that interacts with nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor corepressor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                  rISSUE-Brain cortex;
MEDLINE-97369492; PubMed-9225980;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 428-613 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE OF 1023-2517 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endocrinol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLRAVQRKARFAKLKSLTPSWLMSVLIKMPPGVTSWINA-----ERRLYLETPIGPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAQYYAIGPLIEQIENMQPIKG-----EKVRQAFIGIMPYYKDHIERIVEI-----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                  hormone receptors.";
docrinol. 10:813-825(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evans R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor) (TRAC) (CTG26).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human).
etazoa; Chordata;
theria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sc1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=7566127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96:3519-3524(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PLPRNEFQRQVWLIFEYPESSG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family
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EMBL; AF113003; i
EMBL; AF125672; i
EMBL; U37146; AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -I- INDUCTION: REGULATED DURING CELL CYCLE PROGRESSION.
-I- INDUCTION: THE UTTERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT ARE DIVIDED INTO THREE INDEPENDANT REPRESSION FUNCTIORS, RD2 AND RD3). THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPTOR-INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION DOMAINS (ID1 AND ID2).
-I- DOMAINS (ID1 AND ID2).
-I- DOMAINS THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED SEQUENCE REFERRED TO AS THE CORNR BOX. THIS MOTIF IS REQUIRED AND SUFFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RARS. SEQUENCES FLANKING THE CORNR BOX DETERMINE NUCLEAR HORMONE RECEPTOR
                                           DOMAIN
VARSPLIC
VARSPLIC
CONFLICT
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIFICITY.

-!- SIMILARITY: CONTAINS 1 SANT-A DOMAIN.

-!- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.

-!- SIMILARITY: CONTAINS 2 CORNR BOXES.

-!- SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTIREPRESSOR.
-I- TISSUE SPECIFICITY: UBIQUITOUS, HIGH LEVELS OF EXPRESSION ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>+ +</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFAC; T04689; -. Genew; HGNC:7673; NCOR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF125672; AAD22973.1
EMBL; U37146; AAC50236.1;
EMBL; S83390; AAB50847.1;
EMBL; U80750; AAB91446.1;
   CONFLICT
                                                                                                                                                                                                            DOMAIN
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Pfam; PF00249; myb_DNA-binding; 2.
SMART; SM0395; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 600848; -
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 uclear protein; Transcription regulation; DNA-binding; Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ROSITE; PS50090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; SMRT/TRAC-2 (SHOWN HERE) AND
TRAC-1; ARE PRODUCED BY ALTERNATIVE SPLICING. TRAC-1 CONTAINS ONLY
THE C-TERMINAL RECEPTOR-INTERACTING DOMAIN AND ACTS AS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DETECTED IN LUNG,
                                                                                                                                                             2353
                                                                                                                                                                                                                                                                                                                                                                                                    Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD20946.1; -.
AAD22973.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  MYB_3; 1
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510
685
1002
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                                                                                                                                                             2398
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                           MISSING (IN REF. 2).
A -> P (IN REF. 2).
SS -> EF (IN REF. 2).
S -> T (IN REF. 2).
MISSING (IN REF. 2).
RRTSRAPIEP -> PEDIPAPTES (
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                                                                                                                                                                                                        POLY-PRO.
POLY-PRO.
POLY-GLY.
                                                                                                                                                            POLY-PRO.
MISSING (IN ISOFORM
MISSING (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                  COLLED COIL (POTENTIAL).
INTERACTION WITH SIN3A/B (BY SIMILARITY).
                                                                                                                                                                                                                                                                                 CORNR BOX OF
                                                                                                                                                                                                                                                                                                                PRO-RICH.
                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                        SANT-A (POTENTIAL).
                                                                                                                                                                                                                                                     POLY-LYS
                                                                                                                                                                                                                                                                     POLY-GLN
-> L (IN REF. 2).
-> F (IN REF. 2).
                                                                                                                  (IN REF. 2)
(IN REF. 2)
(IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions on in
                                                                                                                                                            TRAC-1).
                              (IN REF.
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SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-Smooth muscle; Tate R.J., Osipenko O.N., Kempsil F.E.J., Gurney A.M.; Tate R.J., Osipenko O.N., Kempsil F.E.J., Gurney A.M.; "Identification of a voltage-gated potassium channel (KV1.5) in rabbit pulmonary artery smooth muscle."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-New Zealand white; TISSUE-Portal vein; STRAIN-New Zealand white; TISSUE-Portal vein; Clement-Chomienne O., Ishii K., Walsh M.P., Cole W.C.; "Rabbit portal vein Kvl.5."; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-Japanese white; TISSUE-Heart; MEDLINE-96032538; PubMed-7556635; Sasaki Y., Ishii K., Nunoki K., Yamagishi T., Taira N.; The voltage-dependent K+ channel (KV1.5) cloned from rabbit heart and facilitation of inactivation of the delayed rectifier current by the rat beta subunit."; TEBS Lett. 372:20-24(1995).	01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Voltage-gated potassium channel protein Kv1.5. KCNA5. Oryctolagus cuniculus (Rabbit). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. NCBI_TaxID-9986;	10 ABIT IK5_RABIT STANDA	221 YKEAQYYAIGP 231 	165 RCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDVLNFLRSGDLPPRERVRAV 220	142 QE 164	99TATQAGHALPLLP 141 TATQAGHALPLLP 141	74 SPPSGQPAAGRVMPGAARRARGMVV	15 PLRRRPLALPALRLG-ELPANQGGTSAASASSGRRSGQAPAGRERVGVEGATALPPAHCL 73	Query Match 6.3%; Score 112; DB 1; Length 2517; Best Local Similarity 21.9%; Pred. No. 4.6; Matches 68; Conservative 23; Mismatches 104; Indels 116; Gaps 1	CONFLICT 817 817 A -> S (IN REF. 2). CONFLICT 889 889 G -> R (IN REF. 2). CONFLICT 1033 1030 SRSPAPPA -> MEAWDAHP (IN REF. 3). CONFLICT 1034 1034 A -> AEKPYFFPA (IN REF. 2). CONFLICT 1894 1894 K -> T (IN REF. 4). CONFLICT 2494 P -> A (IN REF. 4). SEQUENCE 2517 AA; 274031 MW; F5805C01761258C0 CRC64;
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Query Match
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Matches 57
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PRINTS; PR0169; KCHANNEL.
PRINTS; PR01512; KV15ANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01496; SHAKERCHANEL.
SMART; SM00225; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000636; Mychannel_nlq, InterPro; IPR003972; Shaker channel_nlq, Pfam; PF00520, ic.
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EMBL; AF056943; AAC13312.1;
EMBL; AF149787; AAD56772.1;
HSSP; Q54397; 1BLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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InterPro; IPR001622; K+channel_pore.
InterPro; IPR004052; KY15channel.
InterPro; IPR003091; K_channel.
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IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
TO SPECIFIC SUBCLIQUAR COMPARTMENTS.
SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
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DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein.

DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE)
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QRVLINISGLRFETQLGTLAQFPNTLLGDPAKRLRYFDPLRNE--YFFDRNRPSFDGILY 161
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                                     EVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSG-RHYIPTDSEGRYFIDRDGTHFGDVLN 204
                                                                                                                 ARRANGMVVVTGREPDSRRQDGAMSSSDAEDD----FLEPATPTATQAGHALPLLPQEFP
                                                                                                                                                        GCSQAAPTAGLGDGSQEPAPRGRGCSARRGAEPGERPLPP----QPP------
                                                                                                                                                                                                GTSAASASSGRRSGQ---APAGR---ERVGVE-GATALPPAHCLSPPSGQPAAGRVMPGA 89
                                                                                                                                                                                                                                                       Similarity
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AAD56772.1; -.
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SEGMENT S2.
SEGMENT S3.
SEGMENT S4.
SEGMENT S5.
SEGMENT S6.
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5; Mismatches
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and expression of cDNA and genomic clones encoding delayed rectifier potassium channels in rat brain.";
Neuron 4:929-939(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Voltage-gated potassium channel protein Kv1.3
                                                                                                                                                                                                                                                                                                                                                                                           clone encoding a lymphocyte potassium J. Immunol. 144:4841-4850(1990).
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Swanson R., Marshall J., Smith J., Williams J.,
Folander K., Luneau C.J., Antanavage J., Oliva C
Bennett C., Stein R.B., Kaczmarek L.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stuchmer W., Ruppersberg J.P., Schroerter K.H., Sakmann B. Stocker M., Glese K.P., Perschke A., Baumann A., Pongs O.; "Molecular basis of functional diversity of voltage-gated channels in mammalian brain.";
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Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
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Douglass J., Osborne P.B., Cai Y.C.,
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Stuehmer W., Ruppersberg J.P., Schroerter K.H., Sakmann
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                                                                        s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Everopean Bioinformatics Institute. There are no restr
                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein.

DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A R IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANN TO SPECIFIC SUBCELLULAR COMPARTMENTS.

DOMAIN: THE SEGMENT S4 IS PROBBLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
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Rodentia;
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Sciurognathi;
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PRINTS; PR01569; I
PRINTS; PR01510;
PRINTS; PR01491;
PRINTS; PR01496;
SMART; SM00225; B
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EMBL;
EMBL;
PIR; S
                 Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                    Voltage-gated potassium SH OR CG12348.
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LI; M30312; AAA42035.1;
BL; M31744; AAA41500.1;
R; S06708; S06708.
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SP; Q54397; IBL8.
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IPR003091;
IPR003131;
IPR003968;
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K_tetra; 1
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M+channel_nlg.
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27.0%;
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Pred. No. 1.7;
24; Mismatches
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SEGMENT S3.
SEGMENT S4.
SEGMENT S5.
SEGMENT S6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GGGDPP--
                                                                                                                                                                                                                                                                                                                                     024277;
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                                                                                                                                                                                                                                                                                                                                             Q9VWZ9;
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(POTENTIAL).
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Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M. Beesen K.Y., Benos P.V., Berman B.P., Bhahdari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunchin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman
                                                                                                                                                                                                                                                                            "Molecular organization of the maternal effect region of the Shaker complex of Drosophila: characterization of an I(A) channel transcript with homology to vertebrate Na(+) channel.";
EMBO J. 6:3419-3479/10897
                                                                                                                                                                                                                                                       Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifter Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., William Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., William Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., William Wan K.H., Doyle C., Baxter E.G., William Wan K.H., William Wan K.H., William Wan K.H., William Wan K.H., William Wan Wan K.H., William Wan Wan W.H., William Wan W.H., William Wan W.H., William Wan W.H., William W.H., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kamb A., Tseng-Crank J., Tanouye M.A. "Multiple products of the Drosophila potassium channel diversity.";
Neuron 1:421-430(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schwarz T.L., Tempel B.L., Papazian D.M., Jan
"Multiple potassium-channel components are pro-
splicing at the Shaker locus in Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pongs O., Kecskemethy N., Mueller R., Krah-Jent Baumann A., Kiltz H.H., Canal I., Llamazares S. "Shaker encodes a family of putative potassium the nervous system of Drosophila."; EMBO J. 7:1087-1096(1988).
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MEDLINE-87273502;
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SEQUENCE FROM N.A
MEDLINE-87292096;
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Pongs O., Kecskem
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                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90166523; PubMed=3272175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 331:137-142(1988).
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              Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  450-534 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
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PubMed=2440582;
L.E., Tanouye M.A.;
terization of Shaker, a Dro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=2441471;
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RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Simpson M., Skupski M.P., Smith T.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ve J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhon M., Zhu S., Zhu X., Smith H.O.,
RA Yelder Sequence of Drosophila melanogaster.";
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
CC ION PERMEABLITY OF EXCITABLE MEMBRANES. ASUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE THROUGH WHICH K.F. IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
                                                                                                                                                                                                                                                                                   FlyBase; FBgn0003380; Sh.
InterPro; IPR000210; ByB_PO2.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR004048; KV11channel.
InterPro; IPR003131; K_tetra.
InterPro; IPR003988; K+channel.
InterPro; IPR003636; M+channel_nlg.
InterPro; IPR003972; Shaker_channel.
                                                                                                                                                                                                  PIR; S00479; S00479.
PIR; S00480; S00480.
PIR; S002284; S00248.
PIR; S00482; S00482.
PIR; S00508; S00508.
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Kimmel B.E., Kodira C.D., Kraft C., Kraviz S., Kup D., Lai Z
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright, it is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute, There are no restuee by non-profit institutions as long as its content
            Pfam; PF00520;
Pfam; PF02214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send
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                                                                                                                                                                                        HSSP;
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ALTERNATIVE PRODUCTS: 6 ISOFORMS; ALPHA/ALADULT, B
POPULATION, GAMMA, DELTA/LARVAL, EPSILON/LARVAL
HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLT
IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAUTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-profit institutions as long and this statement is not removed
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Kalush F., Ka
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Kodira C.
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          ion_trans;
K_tetra; 1.
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ES OF POSITIVELY CHARGED AMINO ACIDS A
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Kennison J.A., 1
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Best Local S
Matches 50
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01-JUL-1989 (Rel. 11,
15-JUN-2002 (Rel. 41,
N-myc proto-oncogene p
MYCN OR NMYC.
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CARBOHYD
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PRINTS; PR01496; SHAKERO
SMART; SM00225; BTB; 1:
Ionic channel; Transmem
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                                                                                                                                                                             FLRSGD---LPPRERVRAVYKEAQYYAIGPLLEQL------ENMQPL-KGEKVR
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50; Conser
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447 278
379 300
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311 311
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381 395
381 395
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CYTOPLASMIC (POTENTIAL).
                                                               STANDARD;
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27.2%;
            protein.
                      Last sequence up
                                         Created)
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Pred. No. 2.3;
Pred. No. 2.3;
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KQLQHPLQHVTQTQLYQQQQQQQQQQQQQGFKQQQQQTQQQL
QQQQSHTINASAAAATSGSGSSGLTMRHNNALAVSIETDV
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N-LINKED (GLCNAC. . ) (POTENTIAL).
MAAVAGLYGLGEDROHRKKQQQQQGHQKEQKEEQKKIA
ERKLQLREQQLQRNSLDGYG -> MTMWQSGGMGGHGSQNN
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ERKLQLREQQLQRNSLDGYG -> MAHITTTHGSLSQATR
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SEQUENCE OF 313-464 FROM N.A
MEDLINE-85215633; PubMed-298
Michitsch R.W., Melera P.W.;
"Nucleotide sequence of the
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Stanton L.W., Schwab M., Bishop J.M.;
"Nucleotide sequence of the human N-myc gene.";
Proc. Natl. Acad. Sci. U.S.A. 83:1772-1776(1986)
                                                                                                                              use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Specific phosphorylation of the acidic protein by casein kinase II."; Eur. J. Biochem. 209:945-950(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification and characterization human N-myc oncogene."; Science 232:768-772(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-86092232;
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EMBL; X03294; CAA27037.1;
EMBL; X03295; CAA27038.1;
EMBL; M13241; AAA36371.1;
EMBL; M13228; AAA36370.1;
                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH
BHLH PROTEIN. BINDS DNA AS AN HETERODIMER WITH MAX.
                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: EXPRESSED DURING FETAL DEVELOPMENT. DISEASE: AMPLIFICATION OF THE N-MYC IS ASSOCIATED WITH VARIETY OF HUMAN TUMORS, MOST FREQUENTLY NEUROBLASTOMA, WHEF LEVEL OF AMPLIFICATION APPEARS TO INCREASE AS THE TUMOR
                                                                                                                                                                           European
                                                                                                                                                                                                                                                       TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.

DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;

WWW-"http://www.infoblogen.fr/services/chromcancer/Genes/NMYC112.html"
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                                                                                                an email to license@isb-sib.ch)
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                                                                                                                                                                           Bioinformatics Institute.
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E., DePinho R.A.,
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                                                                                                                  license agreement (See http://www.isb-sib
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                ALT_INIT
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CONFLICT
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01-NOV-1997
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                     Rattus norvegicus (Rat)
                              5E5 antigen.
                                                                                 5E5_RAT
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PROSITE; PS50888; HLH_2; 1.
Nuclear protein; DNA-binding;
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         Eukaryota;
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Y00664; CAA68678.1; ALT_INIT
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 ; Metazoa;
Eutheria;
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 Chordata;
Rodentia;
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19.4%;
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Last
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annotation
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Pred. No. 1.
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I -> V (IN REF.
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HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
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Craniata; Vert
Sciurognathi;
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          Vertebrata;
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Matches 52
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J. Biochem. 118:122-128(1995).
-i- FUNCTION: MIGHT HAVE DNA-BINDING AB--i- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-kpR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Voltage-gated potassium channel protein Kv1.2
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Eukaryota; Metazoa;
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[1]
                                                                                                                                                     expression.";
                                                                                                                                                                                                                Ramaswam1 M., Gautam M., Kamb A., Rudy B., Mathew M.K.;
                                                                                                                                                                                                                                                                  TISSUE-Brain;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96015159; PubMed-8537300;
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                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                       Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            707
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                      . Cell. Neurosci. 1:214-223(1990).

FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQRPSPFAPQEEGLRAESCYDDGAIAPDTDTAS-----GEVPEAGP 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTGREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPEVVP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QRQRLWRQFRVGGGFPPPPTRPPPVLLPLLRLTCAGDPGASR---PGSRRPARRPRGELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEEAQDGLLPRGRDRLPLRPGDSNQRVERPGHPRGGHGAINAPSAPDASPPHHPRRWVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGGRGRGRGGRRGSGLSGTREDAGSPSARRGEQRRRGHGPPAAGAAQVSTRGRRARGQRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUKIV)
                                                                                                                                                                                       potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity

y; Nuclear protein; Antigen.
825 AA; 86831 MW; AF667FE2FD555BDF CRC64;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                 channel genes:
                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
  IN ACCORDANCE WITH THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 105.5;
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                    molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M1smatches
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NA for a possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABILITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₹
                                                                                                                                                                                 cloning and functional
                                                                                                                                                                                                                                                                                                                                                                              Hominidae;
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                                                                                                                                                                                                                                      Tanouye M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RBK2) (HBK5) (NGK1)
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                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
  ELECTROCHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K., Akagawa
DNA-binding
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Best Local
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TRANSMEM 1
TRANSMEM 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                             TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00169; KCHANNEL.
PRINTS; PR01509; KV12CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00520; lon_trans; Pfam; PF02214; K_tetra; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L02752; AAA36141.1;
HSSP; Q54397; 1BL8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                          MOD_RES
                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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125
                      236
                                                                                                                     124 EPATPTATQAGHAL----PLLPQEFPEVVPLNIGGAHFTTRLSTLRCYEDTMLA-AMFSG
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SUBGELLULAR LOCATION: Integral membrane protein.

DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING TI RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY;
IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CH TO SPECIFIC SUBCELLULAR COMPARTMENTS.

DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
                                                                                              7
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SIMILARITY: THIS CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY
                                                                                             DPADEAAALPGHPQDTYDPEADHECCERVVINISGLRFETQLKTLAQFPETLLGDPKKRM
                                                                     RHYIPTDSEGRYFIDRDGTHFGDVLNFLRSGD---LPPRERVRAVYKEAQYYAIGPLLEQ
MFREDEGYIKEEERPLPENEFQRQVWL
                                             RYFDPLRNE - - YFFDRNRPSFDAILYYYQSGGRLRRPVNVPLDIFSEEIRFYELGEEAME
                                                                                                                                                                                                                                                                                                                                channe.
                                                                                                                                             l Similarity
41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC: 6220;
                                                                                                                                                                                                                                                                                                                                                       PR01491; KVCHANNEL.
PR01496; SHAKERCHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR003131;
IPR003968;
IPR000636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001622;
IPR004049;
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                                                                                                                                                                                                                                                     164 182
164 223
222 243
222 275
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293 311
328 347
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                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                Transmembrane;
                     ENMOPL-KGEKVROAFL
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                                                                                                                                                                                                                                                                                                                    family;
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SEGMENT S1.
SEGMENT S2.
SEGMENT S3.
SEGMENT S4.
SEGMENT S4.
SEGMENT S6.
SEGMENT S6.
SEGMENT S6.
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Pred. No. 2
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                                                                                                                                                                                                          PHOSPHORYLATION
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                                                                                                                                              Mismatches
                      252
151
                                                                                                                                                                                                                                                                                                                              transport; Voltage-gated channel;
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                                                                                                                                             Indels
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Search completed: February Job time : 19 secs

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Result
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Maximum
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Perfect score:
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Match
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US-10-024-579-16
US-10-024-579-14
US-10-024-579-12
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Sequence 12, Appl
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	
92.5	92.5	92.5	92.5	93	93.5	94.5	96.5	96.5	96.5	97	97	97	98	98.5	98.5	100	100.5	100.5	101	101.5	101.5	102	104.5	105.5	108	
5.2	5. 2	5.2	5.2	5.2	5.3	5. 3	5.4	5.4	5.4	ت. 4.	5.4	5.4	5 5	5. 5	ۍ ن	5. 6	5	5	5.7	5.7	5.7	5.7	5.9	5.9	6.1	
739	739	739	365	566	. 332	7968	1702	1702	454	456	456	456	687	902	874	580	527	527	399	261	261	275	447	254	351	
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US-10-121-049-478	US-10-028-072-478	US-09-974-298-159	US-10-108-605-343	US-09-797-500-2	US-09-764-868-1013	US-10-077-130-5	US-09-738-973-434	US-09-854-133-434	US-09-993-811-12	US-09-974-712-2	US-09-993-811-2	us-09-989-920-175	US-09-764-868-661	US-09-950-370-12	US09-950-370-2	US-09-925-301-943	US-09-738-973-216	US-09-854-133-216	US-09-893-737-10	US-09-438-486-174	US-09-843-676-174	US-09-737-149-10	US-09-975-719-351	US-09-738-626-6616	US-09-350-874-61	
	•	Sequence 159, App	34	Sequence 2, Appli	Sequence 1013, Ap	Sequence 5, Appli	Sequence 434, App	Sequence 434, App	Sequence 12, Appl	Sequence 2, Appli	Sequence 2, Appl1	Sequence 175, App.	Sequence 661, App	Sequence 12, Appl	Sequence 2, Appli	Sequence 943, App	Sequence 216, App	16,	Sequence 10, Appl	174,	74,	Sequence 10, Appl	351,	Sequence 6616, Ap	Sequence 61, Appl	

ALIGNMENTS

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RESULT 2
US-10-024-579-7
; Sequence 7, Application US/10024579
; Patent No. US20020119522A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT; ORGANISM: homo sapiens US-10-024-579-5
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US-10-024-579-5
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APPLICANT: Gerhardt, Brenda
APPLICANT: Hibun, Erin
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020119522A1el Human Ion Channel-Related Proteins
TITLE OF INVENTION: and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0274-USA
CURRENT APPLICATION NUMBER: US/10/024,579
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/258,595
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEC.
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 110; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 5
LENGTH: 120
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SOFTWARE: FastSEQ for
                                                                                                                                                                156 HFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDV----LNF-LRSGD 210
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                                                                                                                                                                                                                                             96 MVVVTGREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPEVVPLNIGGA | 155
                                                                                                                                                                                                                      1 MVVVTGREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPEVVPLNIGGA 60
                                                                                                                                          HFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGYVSPSTINFVVLAGD
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Pred. No. 3.5e
3; Mismatches
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; LENGTH: 106
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-024-579-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: LEX-0274-USA
CURRENT APPLICATION NUMBER: US/10/024,579
CURRENT FILING DATE: 2001-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/258,595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILE REFERENCE: Aeomica-X-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIOR APPLICATION NUMBER: US 60/180,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 ----LNF-LRSGD 210
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                         APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04 APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                   APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                       APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                         FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00664
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5. US20020048763A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/864,761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVENTION: No. US20020119522Alel Human Ion Channel-Related Proteins
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                                                                                                   2001-01-30
                                                                                                                                                                                                                               2001-01-30
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83.6%;
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Pred. No. 1.2e-19;
5; Mismatches 2
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                                                                                                                              NAME/KEY: SITE LOCATION: (168)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino US-09-925-299-879
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 1556
                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/US00/05883 PRIOR FILING DATE: 2000-03-08
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                                                                                                                                                                                                                                                                                                                                   RIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       TILE REFERENCE: PA102
                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: Rosen et al.
                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                  TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 FPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHF 199
                             108 RQDGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPEVVPLNIGGAHFTTRLSTLRCY 167
12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/234,687
RPVGRMTSQTPLPQSPRPRRPTMS-
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56; Conservative
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100.08; Pi
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pred. No. 3.3
0; Mismatches
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HIT: Q13829,
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                                                                               Score 245;
Pred. No. 1
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TYPE: PRT
ORGANISM: homo sapiens
US-10-024-579-16
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                             SEQ ID NO 14
LENGTH: 257
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/10024579 Patent No. US20020119522A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gerhardt, Brenda
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICATION: No. US20020119522A1e1 Human Ion Channel-Related Proteins
TITLE OF INVENTION: and Polyuncleotides Encoding the Same
FILE REFERENCE: LEX-0274-USA
CURRENT APPLICATION NUMBER: US/10/024,579
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/258,595
PRIOR EPILING DATE: 2000-12-28
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                                                                                                                                                           APPLICANT: Gerhardt, Brenda
APPLICANT: Hilbun, E-in
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Usexander Jr.
TITLE OF INVENTION: NO. US20020119522A1e1 Human Ion Channel-Related
TITLE OF INVENTION: and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0274-USA
CURRENT APPLICATION NUMBER: US/10/024,579
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/258,595
PRIOR APPLICATION NUMBER: US 60/258,595
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEC ID NOTE: 1000-12-28
NUMBER OF SEC ID NOTE: 1000-12-28
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APPLICANT: Gerhardt, Brenda
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexand
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                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                         NUMBER OF SEQ ID NOS:
ORGANISM: homo sapiens
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 264
TYPE: PRT
ORGANISM: homo sapiens
US-10-024-579-12
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US-10-024-579-12
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APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Exenda
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: TIVENTION: No. US20020119522Alel Human Ion Channel-Related Proteins
TITLE OF INVENTION: and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0274-USA
CURRENT APPLICANTION NUMBER: US/10/024,579
CURRENT FILING DATE: 2001-12-18
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Best Local Similarity
Matches 45; Conserva
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Best Local Similarity 35.2%;
                APPLICANT: Gerhardt, Brenda
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANTINIENTION: No. US20020119522A1el Human Ion
TITLE OF INVENTION: and Polynucleotides Encoding th
FILE REFERENCE: LEX-0274-USA
                                                                                                       APPLICANT: Friddle, Carl Johan
APPLICANT: Gerhardt, Brenda
APPLICANT: Hilbun, Erin
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CURRENT APPLICATION NUMBER: US/10/024,579
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35.2%; Pred. No. 2.2e-
ltive 28; Mismatches
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Pred. No. 2.1
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                                                                Channel-Related
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NUMBER OF SEQ ID NOS: 17
SECTIVARE: FASTSEQ FOR WIT
SEQ ID NO 10
LENGTH: 283
TYPE: PRT
ORGANISM: homo sapiens
US-10-024-579-10
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: LOCATION: (358)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1240
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Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
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Best Local Similarity 35.2%; Pred. No. 2.4
Matches 45; Conservative 28; Mismatches
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LENGTH: 378
                                                                                                                                                                                                                                                Matches
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SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2001-01-17
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PRIOR APPLICATION NUMBER: US 60/258,595
PRIOR FILING DATE: 2000-12-28
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                      140 LPQEFPEVVPLNIGGAHFTTRLSTLRCYE-DTMLAAMF--SGRHYIPTDSEGRYFIDRDG 196
                                                                                                                      106 ---SRRQDGAMSSS------DAEDD-----FLEPATPTATQAGHALPL 139
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LLGFHTDWLTLNVGGRYFTTTRSTLVNKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSP 161
                                                                               LSVAXSKLGIKATSVYNGKGGLIDDIALIXDDDVLFVCEGEPFIDPQTDSKPPEG-----
                                                                                                                                                                GGGPGGR----
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Pred. No. 1e-05;
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; ORGANISM: human
US-10-062-879-4
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Best Local Similarity 37.7%;
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                                                                                                                       Query Match
                                                                                                                                                                                                                                                  SEQ ID NO 4
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                                                                                    Matches
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Patent No. US20020127649A1
                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Human Potassium Channel Polynucleotides TITLE OF INVENTION: Polypeptides and Uses Therefor FILE REFERENCE: ahp-98089
CURRENT APPLICATION NUMBER: US/10/062,379
CURRENT FILING DATE: 2002-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/258,595
PRIOR FILING DATE: 2000-12-28
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-1
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                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cockett, Mark I.
APPLICANT: Dilks, Daniel W.
APPLICANT: Chang Ling, Huai-Ping
APPLICANT: Sokol, Patricia T.
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APPLICANT: Turner, C. Alexander Jr.
HITLE OF INVENTION: NO. US20020119522Alel Human Ion
TITLE OF INVENTION: and Polynucleotides Encoding ti
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                                                                                                                                                                                                                              ENGTH: 636
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                                    137 LPLLP----QEFPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 DVLNFLRSGD-LPPRE--RVRAVYKEAQYYAIGPLLEOLEN--MQP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 EVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSE----GRYFIDRDGTHFG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 FILDFLRTHQLLLPTEFSDYLRLQREALFYELRSLVDLLNPYLLQP 105
                                                                                  Local Similarity
les 35; Conserv
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MPLAPADKNKRQDELIVLNVSGRRFQTWRTTLERYPDTLLGS--TEKEFFFNEDTKEYFF 84
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                                                                                    Conservative
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Pred. No. 0.00011;
18; Mismatches 33;
                                                                                Score 127; DB 12;
Pred. No. 0.0065;
.5; Mismatches 43
                                                                                                                         Length 636;
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; ORGANISM: human
US-10-062-879-2
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LENGTH: 532
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SEQ ID NO 2
LENGTH: 655
                                                                                                                                              Matches
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09993811
Patent No. US20020119476A1
GENERAL INFORMATION:
APPLICANT: Pharmacia AB
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                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleotide Sequences FILE REFERENCE: 00248
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/993,811
CURRENT FILING DATE: 2001-11-16
                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0
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PRIOR FILING DATE: 1998-10-23
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CURRENT FILING DATE: 2002-01-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cockett, Mark I.
APPLICANT: Dilks, Daniel W
APPLICANT: Chang Ling, Hua
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 13
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                              104 PDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPEVVPLNIGGAHFTTRLST 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 LPLLP----QEFPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFI 192
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   69 PFTGR------
                                                                       11 GKAPGGSVSTGVGTAEGAPSPAGVTPPPPPPRP--GRTFHAIFTRRHRTPDWGGCGVGATR 68
                                                                                                       50 GQAPAGRERYGYEGATALP-PAHCLSPPSGQPAAGRYMPGA-ARRAR----GMYVYTGRE 103
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                                                                                                                                                               Local Similarity
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Chang Ling, Huai-Ping
Sokol, Patricia T.
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34.7%; Pred. No. 0.0068;
-----PGCARHGATVPAALRCCERLV-LNVAGLRFETRART 108
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                                                                                                                                                             Score 120.5; DB Pred. No. 0.018;
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SEQ ID NO 3
                                                                                                                                                                                                               Sequence 3, Application US/09795668 Patent No. US20020045577A1
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Best Local
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Patent No. US20020165144A1
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                                                                                                                                                                                            GENERAL INFORMATION:
                                  APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
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PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
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CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/795,668
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                                                                                                                                                  APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
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NUMBER OF SEQ
                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 418
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                                                                                                                                                                                                                                                                                                                                 DANSTSRAPAAFRA-SFPPLETGRNLKKEVSRVLCKRCALPPRLKEMKSQESAAGSKL
                                                                                                                                                                                                                                                                                                                                                                   DGTHFGDVLNFLRSGDLPPRERVRAVYKE-----AQYYAIGPLLEQLENMQPLKGEKV 247
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24.58;
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; SEQ ID NO 3
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-668-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.4%; Score 113.5; DB 10; Length 418; Best Local Similarity 24.5%; Pred. No. 0.051; Matches 73; Conservative 31; Mismatches 93; Indels 101; Gaps
                         195 DGTHFGDVLNELRSGDLPPRERVRAVYKE-----AQYYAIGPLLEQLENMQPLKGEKV 247
                                                                                                                                                         145 PEVVPLNIGG----AHETTRLSTLRCYEDTMLAAMESGRHYIPT-----DSEGRYFIDR 194
208 DANSTSRAPAAFRA-SFPPLETGRNLKKEVSRVLCKRCALPPRLKEMKSQESAAGSKL 264
                                                                                                         161 HOVWAVKAGGLKKDSLLTVRLGTW-----
                                                                                                                                                                                                               102 GEAGAWGGDREPPAAGPRALGPPAEEPLLAANGTVPSWPTAPVPSAGEPGEEAPYL-VKV 160
                                                                                                                                                                                                                                                                                                                            57 -----ASVCSPPS----VGSVQELAQRAA---VVIEGKVHPQRRQQGALDRKAAAAA 101
                                                                                                                                                                                                                                                                                                                                                                               62 EGATALPPAHCLSPPSGQPAAGRVMPGAARRARGMVVVTGREPDSRRQDGAMS------ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                  --SSDAEDDFLE-----PATPTAT-----QAGHALFLLPQEF 144
                                                                                                         ----GHPAFPSCGRLKEDSRYIFFMEP 207
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Search completed: February 12, 2003, 11:09:42
Job time: 15 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:07:30 ; Search time 21 Seconds (without alignments)
1570.196 Million cell updates/sec

Title: US-10-086-156-24 1780 1 MTMAVLRNRKGGKG

Perfect score:

șequence: MTMAVLRNRKGGKGPLRRRP......NNEKKSPVQLPAGVFQHFMG

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*

pir1:*
pir2:*
pir3:*

Pred. No. is the number of results predicted by chance score greater than or equal to the score of the result and is derived by analysis of the total score distribut distribution to have a being printed,

SUMMARIES

Result

Query

29	28	27	26	25	24	23	22	21	.20	19	18	17	16	15	14	13	12	1	10	و ا	œ	7	6	u	4	ω	2	٦	ĕ
117.5	118	121	121	121	121	121.5	123	123	123	124.5	127	130.5	131	131	131.5	132	132	132.5	134	134	137.5	143	143.5	144.5	146.5	160.5	175	200	Score
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155	139	630	602	514	490	326	460	460	207	272	236	261	244	220	246	670	179	140	231	208	204	190	373	212	651	134	348	220	Length
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ALIGNMENTS

Query Match 11.2%; Score 200; DB 2; Length 220; Dest Local Similarity 35.6%; Pred. No. 1.1e-07; Matches 64; Conservative 22; Mismatches 46; Indels	RESULT 1 T20366 hypothetical protein D2045.8 - Caenorhabditis elegans C;Becies: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T20366 R;Lloyd, C. submitted to the EMBL Data Library, August 1994 A;Reference number: Z19262 A;Accession: T20366 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-220 (WIL) A;Cross-references: EMBL:Z35639; PIDN:CAA84696.1; GSPDB:GN00021; CESP:D2045.8 A;Experimental Source: clone D2045 C;Genetics: A;Gene: CESP:D2045.8 A;Map position: 3 A;Introns: 39/3; 127/3; 169/1; 194/3	
DB 2; Length 22 le-07; s 46; Indels	elegans 1999 #text_chang	
48;	a 15-Oct	
Gaps	L-1999 L-1999	
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Ş A; Accession: A41784 A; Molecule type: mRNA A; Residues: 1-348 <WOL> C;Accession: A41784 R;Wolf, F.W.; Marks, R.M.; Sarma, V.; Byers, M.G.; Katz, R.W.; Shows, T.B.; Dixit, V., J. Biol. Chem. 267, 1317-1326, 1992 A;Title: Characterization of a novel tumor necrosis factor-alpha-induced endothelial A;Reference number: A41784; MUID:92112779; PMID:1370465 tumor necrosis factor-alpha-induced protein B12 - human C;Species: Homo sapiens (man) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Aug-1997 밁 Š 밁 δÃ В 240 QPLKGEKVRQAFIGIMPYYKDHLERIVEIAFLRAVQRKARFAKLKSLIPSWLMSVLIKMP 183 PTDSEGRYFIDRDGTHFGDVLNFLRSGD--LPPRER-VRAVYKEAQYYAIGPLLEQLENM 123 LEPATPTATQAGHALPLLPQEFPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYI 96 --LCGERLEOS---LNPYY--HLVSTV----LEA--RKIIFATEKPI-----41 _ sequence extracted from NCBI backbone (NCBIN:76547, NCBIP:76550) it is uncertain whether Met-1 or Met-33 is the initiator TKNEEGSVFIDRDSKHFRLILNFLRDGQIALPDSDREVREVLAEASYFLLDPLIE----MEPST-----------IVKLDVGGKIFKTTIFTL-CKHDSMLKTMFCTDVPV -WLRLP 299 239 40 182 135 95

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C;Accession: A39372
R;Pak, M.D.; Baker, K.; Covarrubias, M.; Butler, A.; Ratcliffe, A.; Salkoff, L.
Proc. Natl. Acad. Sci. U.S.A. 88, 4386-4390, 1991
A;Title: mShal, a subfamily of A-type K(+) channel cloned from mammalian brain.
A;Reference number: A39372; MUID:91239573; PMID:2034678
A;Status: preliminary
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A; Map position: 17q22-17q23
A; Start codon: CTG
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A39372
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                                                                                                                                     potassium channel protein Shall - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 05-Nov-1999
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A; Gene: GDB: TNFAIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F23E5.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description: The sequence; Reference number: Z21119; Accession: T32065
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: CESP:F22E5.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:AF016681; PIDN:AAB66174.1; GSPDB:GN00020; CESP:F22E5.8 Experimental source: strain Bristol N2; clone F22E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: DNA
Residues: 1-134 <GRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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Local Similarity 31.7%;
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                                                                                                                                                                                                                                                                                     IENDSQLLQILAAQQKVSFDKI 133
                                                                                                                                                                                                                                                                                                                           LERIVEIARLRAVORKARFAKL
                                                                                                                                                                                                                                                                                                                                                                     MRDGDVVLPSCELTVKELLAEAQFYLLDELIELCSLKIEPVQAPKIKLRF---
                                                                                                                                                                                                                                                                                                                                                                                                       LRSGD--LPPRE-RVRAVYKEAQYYAIGPLLEQLE-NMQPLKGEKVRQAFLGLMPYYKDH 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETVQLDVGGTIFKTSKSTLTKF-NGFLKIMLESDIGLKIDESGSIFIDRSPKHFDLILNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLIE 183
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                                                                                                                                                                                                                                                                                                                             283
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Pred. No. 5e-05;
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Pred. No. 1.4e-05;
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A; Residues: 1-651 < PAK>
                                                                                                                                                 hypothetical protein F18A11.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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                                                                                            R; Wallis, J.
submitted to the EMBL Data
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A; Introns: 40/3; 121/3; 160/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein B0281.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-373 <WIL>
                                                       A; Reference number: A; Accession: T26685
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A; Reference number: Z21109
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                                                                                                                                                                                                                                                                                     124 VVIHYLAYKNQLHTI 138
                                                                                                                                                                                                                                                                                                                        257
                                                                                                                                                                                                                                                                                                                                                                                                 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 VVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDVLNFL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 DRK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 PLKGEKVRQAFLGLMPYYKDHLERIVE
                                                                                                                                                                                                                                                                                                                                                              64
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                                                                                                                                                                                                                                                                                                                        ----YYKDHLERI 265
                                                                                                                                                                                                                                                                                                                                                          RSGDVDLPDSENELKELKREAEYYSLEKLATLCQSSMPKIKSYKTADELLNMIANTKKVV
                                                                                                                                                                                                                                                                                                                                                                                               RSG--DLPPRE-RVRAVYKEAQYYAIGPLLEQLENMQP-LKGEKVRQAFLGLMP----- 256
                                                                                                                                                                                                                                                                                                                                                                                                                                     IVKLNVGGTVFVTLKSTLTKHHGIFKALV---KTEMPAEDGDSFFIDRSPKHFETVLNYI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESGEYFFDRDPDMFRHVLNFYRTGRLHCPRQECIQAFDEELAFYGLVPELVGDCCLEEYR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPLAQQPLPPAPEVKASRGDEVLVVNVSGRRFETWKNTLDRYPDTLLGS--SEKEFFYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.1%;
1 Similarity 30.4%;
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                 #sequence_revision 15-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTD | 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.2%; Score 146.5; 31.3%; Pred. No. 0.(
                                                                                          Library, October 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            score 144.5;pred. No. 0.0023; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elegans cosmid B0281
                                     from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          July 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 0.0014;
52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
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A; Map position: 2
A; Introns: 38/3; 115/3; 135/1
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C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A: Introns: 7/3;
                                                                                                                                                                                                                                                                                               hypothetical protein ZC239.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                                                                                             A; Reference number: Z20117
A; Accession: T25972
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                               A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :Experimental source:
                                                                                                                                                                                                              ;Wu, X.; Kramer, J.

ubmitted to the EMBL Data Library, December 1996,
Description: The sequence of C. elegans cosmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ubmitted to the EMBL Data Library, Reference number: Z20135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Reference number:
;Accession: T26019
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession:
                                                                                                                                                                                                                                                                                 Accession: T2597
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                                         Gene: CESP:ZC239.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 GDVLNFLRSGDLPPRERVRAVYK---EAQYYAI---GPLLEQLENMOP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 EVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSG-----RHYIPTDSEGRYFIDRDGTHF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 LRSGD--LPP--RERVRAVYKEAQYYAIGPLLEQL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 EVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDVLNF 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                              66 AYVLHFLRTDKLSLPEQFREVARLKDEADFYRLERFSTLLSNASSISP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 LRDGDHFVAPSDTEACDELKREAHFYNM-PFLAEM 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 DVITLNVGGTMYTTTRSTLSKETDTLLANIASGSLSEDEQANVVTLPDGTLFVDRDGPLF
                                                                                                                                                             preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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43.2%; Pred. No. 0.00
tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 143; DB 2;
Pred. No. 0.0015;
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                                                                                                                                                                                                                       ZC239
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                                                                                                   CESP: ZC239.5
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A;Map position: 2
A;Introns: 37/3; 133/3; 175/1
A;Introns: 37/3; 133/3; 175/1
C:Superfamily: Caenorhabditis elegans hypothetical protein ZC239.
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submitted to the EMBL Data Library, Decemb
A;Description: The sequence of C. elegans
A;Tescription: Z20117
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    A;Gene: CESP:F22E5.6
A;Map position: 2
                                                                                                                                                    R;Graves, T.; Wohldmann, P.; Clarke, K.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans coss
A;Reference number: Z21119
A;Accession: T32070
                                                                                                                                                                                                                                                                                     hypothetical protein F22E5.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U80842; PIDN:AAB37941.1; GSPDB:GN00020; A;Experimental source: strain Bristol N2; clone ZC239
                                                        A; Experimental source:
                                                                            A; Cross-references:
                                                                                            A; Molecule type: DNA
A; Residues: 1-231 <GRA>
                                                                                                                                    A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA
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                                                                                                                                                                                                                                                                     Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 EVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDVLNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 YKDHLERIVEI 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 VLNFLRSG--DLPPR-ERVRAVYKEAQYYAIGPLLEQLEN-MQPLKGEKVRQAFLGLMPY
                                                                                                                                                                                                                                                                                                                                                                                                             62
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                                                                                                                                preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                           MRDGCLALPKNERDLTELMAEAQYYLLDGLIDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                               LRSG--DLPPRER-VRAVYKEAQYYAIGPLLEQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                               dmann, P.; Clarke, K.
                                                      EMBL:AF016681; PIDN:AAB66172.1; G
ce: strain Bristol N2; clone F22E5
                                                                                                                                    translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 134;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 137.5; DB Pred. No. 0.0043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   December 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cosmid ZC239.
                                                                                                                                                                                          cosmid F22E5
                                                                                                                                                                                                                                                                                                                                                                                                                                               236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
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                                                                          GSPDB:GN00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 208;
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                                                                          CESP: F22E5.6
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Introns: 40/3; 125/3; 170/1

Indels

10;

Gaps

29-Oct-1999

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submitted to the EMBL Data Library, December 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, October 1998
A; Description: The sequence of C. elegans cosmid C40A11.
A; Reference number: 221374
A; Accession: T33590
                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C40A11.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
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A; Introns: 37/3; 132/1
                                                                                                                                                                    A; Experimental source:
                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-179 < MAG>
                                                                                                                                                                                                                                                                                                                                                   R; Maggi, L.; Goela, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily:
                                                                                                       A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ZC239.14 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reference number: Z20117
                                                             Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12
                                                                                                                                                                  ;Cross-references: EMBL:AF099914; PIDN:AAC68757.1; GSPDB:GN00020; CESP:C40A11.6;Experimental source: strain Bristol N2; clone C40A11
                                                                                                                                                                                                                                              Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                         Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA
Residues: 1-140 <WUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: CESP: ZC239.14
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                           Query Match
                                                                                      Introns: 40/3;
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: EMBL:U80842; PIDN:AAB37956.1; GSPDB:GN00020; CESP:ZC239.14
Experimental source: strain Bristol N2; clone ZC239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 EVVPLNIGGAHETTRLSTLRCYE---DTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 LNFLRSGD--LPPRE-RVRAVYKEAQYYAIGPLLEQLEN-MQPLKGEKV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 LRSG---DLPP--RERVRAVYKEAQYYAIGPLLE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
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                                                                                                                            CESP:C40All.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 EIVKLDVGGTIFKTSKSTLTKFNGFFKTMLECDIG----LKLDESGCIFIDRSPKHFDLI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDVLNF 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKIRLNIGGTIFETSKSTLIKF-DGFFKTLLETDIPIQKDDSNCIFIDRSPRHFEKILNY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNEWRDGDVALPNCELKLKELLVEAQFYLLDGLIEMCNSKIMPVEPPKL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity
37; Conserv
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                                                                                      123/3
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      7.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 134; DB 2;
Pred. No. 0.0092;
      Score
Pred.
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      132; DB 2;
No. 0.0093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 231;
                       Length 179;
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                                                                                                                                                                                                                     A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule: 1-246 < MUX>
A; Residues: 1-246 < MUX>
A; Cross-references: EMBL: U80842; PIDN: AAB37955.1; GSPDB: GN00020;
A; Cross-references: Strain Bristol N2; clone ZC239
                                                                                                                                                                                                                                                                                                                                                                                 R;Wu, X.; Kramer, J.
submitted to the EMBL Data Library,
when the sequence of C. e
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A; Introns: 87/2;
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                                                                                                                                                              A; Map position: 2
A; Introns: 37/3; 127/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein ZC239.15 - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T23B12.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
                                                                                                                                                                                                        A;Gene: CESP:ZC239.15
                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                  A; Description: The sequence A; Reference number: Z20117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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Residues: 1-670 <DAV>
                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Caenorhabditis elegans
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Experimental source:
146 EVVPLNIGGAHFTTRLSTLRCYE---DTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 VVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDVLNFL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 VVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDVLNFL 206
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                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTKQVDLCGIKVDTLKHEALFFGLTPLIRRLTLCEELSSTSCGSVYFCGMIP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSGDLP-PRERVRAVYKEAQYYAIGPLLEQLENMQPLKGEKVRQA-FLGLMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSGVTVLPDSEKELQELKKEAEFY-----LLEHLVDLCEPIK-NKIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSG--DLPPRER-VRAVYKEAQYYAIGPLLEQLENM-QPLKGEKVR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVKLNVGGSVFETWKSTL-TKQDGFFKTLIETNVPVKKDTSDCYFIDRSPKYFETVLNYM 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39;
                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence nber: Z21137
                                                                                                                                           Caenorhabditis elegans hypothetical protein ZC239.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185/3; 293/1; 400/1; 457/1; 540/2;
                                                               Conservative
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Pred. No. 0.015;
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Pred. No. 0.05;
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Indels Length

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Gaps

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A;Introns: 40/3; 123/3; 162/1
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12
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C;Species: Caenorhabditis elegans
C;sate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
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Best Local Similarity 31...
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bmitted to the EMBL Data Library, October 1998
Description: The sequence of C. elegans cosmid C40All.
Reference number: 221374
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esidues: 1-220 <WAG>
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	032) L	2 0	1 1	212	651	647	647	234	276	234	325	290	247	435	234	815	815	234	259	259	316	730	283	704	259	707	707	298	228
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	Q8uw33 ga	-0	CONT. Car			S	075671 homo	Q9nsa2 homo	Q9nxv2 homo		Q8vc57 mus		095517 homo	Q96g52 homo	Q9p2m9 homo	Q96n73 homo				Q9d7x1 mus	Q8wvf5 homo	070479 mus				_	Q8tbc3 homo	5	S	Q9vdh3 dro
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ALIGNMENTS

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Best Local Similarity
Matches 189; Conser
                                                                                                                                                                       Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Kawakami E "NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO5631; BAB71236.1;
InterPro; IPR003131; K.tetra.
InterPro; IPR003580; Protachykinin.
Pfam; PF02214; K.tetra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q96MP8 PRELIMINARY; PRT; 289 AA.
Q96MP8; O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FL/32069 fis, clone CCBBF1000118, weakly simil necrosis factor, alpha-induced protein 1, endotheli
                                                                                                                                    Pfam; PF02214; K_tetra; 1.
SMART; SM00203; TK; 1.
SEQUENCE 289 AA; 33132 !
                                                                                                                                                                                                                                                                                                                                  Oshima A., Takahashi.Fujii A., Tanase T., Imose N., Takeuchi
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie
Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                 Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda
Yagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B.,∣
                  96 MVVVTGREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPEVVPLNIGGA
 MVVVTGREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPEVVPLNIGGA
                                                                      Conservative
                                                            55.1%; bc.
100.0%; Pr
                                                                                                                                          33132 MW;
                                                                Score 981; DB 4; I
Pred. No. 1.7e-66;
D; Mismatches 0;
                                                                                                                                        1F0D1F618CD5E459 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   weakly similar 1, endothelial.
                                                                                                   Length 289;
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RESULT QUENTING CO.
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Best Local Similarity
Matches 113; Conserv
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                                                                                                                                                                                     Q9BQ13;
                                                                                                                                                                                                                                                                                                                                                                                                                                    libraries.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB056802; BAB39326.1; -.
InterPro; IPR003131; K.tetra.
                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 18, Last annotation update)
Unknown (protein for MGC:3993) (protein for MGC:2376).
  SEQUENCE FROM N.A
                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09BE68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9BE68
                        Submitted (JAN-2001)
                                     Strausberg R.;
                                                             SEQUENCE FROM N.A.
                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-FRONTAL LOBE LEFT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9541;
                                                 TISSUE-LUNG;
                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                             MLAAMFSGRHYIPTDSEGRYFIDRDGTHFGDVLNFLRSGDLPPRERVRAVYKEAQYYAIG 230
                                                                                                                                                                                                                                                                            PLLEQLENMQPLKGEKVRQAFLGLMPYYKDHLERIVEIARLRAVQRKARFAKLK 284
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                                                                                                                                                                                                                                                              PLLEQLENMQPLKGEKVRQAFLGLMPYYKDHLERIVEIARLRAVQRKARFAKLK 114
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                                                                                                                                                                                                                                                                                                                                                                32.8%;
larity 99.1%;
Conservative
                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                 Chordata;
Primates;
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                        the EMBL/GenBank/DDBJ databases
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                 Craniata; Vo
Catarrhini;
                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 FBD124ABB711EB85 CRC64
                                                                                                                                                                                                                                                                                                                                                                          584; DB 6;
No. 1.3e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 AA
                                                                                                              Vertebrata; Euteleostomi;
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RESULT 4
Q9CU79
ID Q9CU
D7 Q9CU
D7 Q9CU
D7 Q1-1
D7 Q1-
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Best Local
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                                                                                                                                                                                                                                                                                                      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M., Guronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Satok H., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Sazuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawai J., bhinggwa A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Gaasterland T., Gissi C., King B., Quackenbush Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pasana Warner L., Washlo
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                       Pfam; PF02214; K_tetra;
SMART; SM00225; BTB; 1.
NON_TER 1
                                                                                                              InterPro;
InterPro;
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InterPro; IPR003131; K_tetra.
Pfam; PF02214; K_tetra; 1.
SMART; SM00225; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI TaxID=10090;
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01-JUN-2001
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                                                                                                                                                                                                                             Nature 409:685-690(200)
                                                                                                                                                                                                                                                                                    Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawai J., Shinagawa A., Shibata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21085660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266
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                                                                                                                                                                                                                                                       Functional annotation of a full-length
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                                                                                                              IPR000210; BTB_POZ. IPR003131; K_tetra.
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     290 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.A.
GJ; TISSUE-HEAD;
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                                                                                                                                                                                                BAB307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed-11217851;
                                                                                                                                                                         5430433B02R1k.
     31443 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17, Created)
17, Last sequence up
17, Last annotation
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Pred.
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     14B511251CE8D005 CRC64;
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No. 4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290
                                                                                                                                                                                                                                                       mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M., Itoh M., Ishii Y., Adachi J., Fukuda S., Kondo S., Yamanaka I., Kasukawa T., Saito R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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Best Local S
Matches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 56; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8R3T6 PRELIMINARY; PRT; 234 AA. Q8R3T6; Q8R3T6; Q1-JUN-2002 (TrEMBLrel. 21, Created) Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update) Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similar to hypothetical protein MGC2376.

Mus musculus (Mouse). Chardata: Cranlata: Vertebrata;
  Q8TCA6
Q8TCA6;
01~JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC024588; AAH24588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 234 AA; 27008 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRRRPLALPALRLGELPANQGG--TSAASASSGRRSGQAPAGRERVGVEGATALPPAHCL
                                                                                                                                                                                                                                                                                                           DYLRTGQV-PTEYVPEVYQEAKFYQIHLLVKILEDMPQIFGEQVARTQFLMGVPNYRENL
                                                                                                                                                                                                                                                                                                                                                           NFLRSGDLPPRERVRAVYKEAQYYAIGPLLEQLENMQPLKGEKV-RQAFLGLMPYYKDHL
                                                                                                                                                                                                                                                                                                                                                                                                                KVVELNVGGQFYTTTMGTLMKHPGSKFSEILSRSARHY - - KDAQGRFFIDRPGTYFGLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                             EVVPLNIGGAHFTTRLSTLRCYEDIMLAAMF -- SGRHYIPTDSEGRYFIDRDGTHFGDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HMMTPETASLLHLWTVRIPPGSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYMM-----SDPVTLNVGGHLYTTSLTTLTRYPDSMLGAMFGGDFPTARDPQGNYFID 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPAS-----
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                                                                                                                                                                                                                                                           ERIVEIARLRAVORKA 278
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(TrEMBLrel.
                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Rodentia;
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Created)
Last sequence update)
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Pred. No. 8e-11;
)7; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 244; DB 11;
Pred. No. 7.9e-11;
4; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                PRT;
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Best Local Similarity
Matches 51; Conser
                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                     Matches
                                                                                                                                                                                                                  Submitted (APR-2001) to the EME
EMBL; BC006935; AAH06935.1; -
InterPro; IPR0002210; BTB_POZ.
InterPro; IPR003131; K_tetra.
Pfam; PF02214; K_tetra; 1.
PROSITE; PS50097; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          Q922M3;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Le Hypothetical 26.5 kDa protein Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel, 19, Created)
01-DEC-2001 (TrEMBLrel, 19, Last sequence update)
01-MAR-2002 (TrEMBLrel, 20, Last annotation update)
Similar to tumor necrosis factor, alpha-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q922M3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 228 AA; 26540 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2002) to the EMBL; BC022893; AAH22893.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-10090;
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KHFGTILNYLRDGGVPLPESRREIEELLAEAKYYLVQGLLEECQ
                                                                                                                            SGQPAAGRVMPGAARRARGMVVVTGREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHA| 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTLNVGGHLYTTSLTTLTRYPDSMLGAMFGGDFPTARDPQGNYF1DRDGPLFRYVLNFLR
                      THEGDYLNELRSGDLP---PRERVRAVYKEAQYYAIGPLLEQLE
                                                                                                   SGDSVVSSAVPAAATRTTSF---KGASPSSK-----
                                                                        LPLLPQEFPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDG
                                                                                                                                                                 Similarity
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                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                         (Mouse)
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                                                 YVKLNVGGALYYTTMQTL-TKQDTMLKAMFSGRMEVLTDSEGWILIDRCG
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                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                    35701 MW;
                                                                                                                                                                11.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.9%;
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Pred. No. 2.
                                                                                                                                                                Score 208; DB 11;
Pred. No. 6.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                      590AEF2D4F22D2D9 CRC64;
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Best Local
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Q9H3F6;
01-MAR-2001
01-MAR-2001
                                                                                 Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.V.
Xu Y.Y. Ye J., Song L., Gao Y., Zhang C.L., Zhang J., V.
Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.J.
Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF113208; AAG39279.1;
InterPro; IPR000210; BYB_POZ.
InterPro; IPR003131; K_tetra.
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SEQUENCE FROM N.A.

Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

"NEDO human cDNA sequencing project.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AK027643; BAB55188.1;

EMBL; AK027643; BAB55188.1;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ14637 fis, clone NT2RP2001327, moderately s
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSTP028
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InterPro; IPR003131; K_tetra.
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                                            Pfam; PF02214; K_tetra; 1.
SMART; SM00225; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
PISSUE-AORTA;
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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PROSITE; PS50097; BTB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGESVVSSAVPAAATRTTSF---KGTSPSSK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
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  PS50097; BTB; 1.
313 AA; 35432
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313 AA;
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                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
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17,
  MW;
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Last sequence update)
Last annotation update)
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Pred. No. 8.6e-08;
                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae,
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  199AF07A30D5BCA6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                               Hominidae;
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                                                                                                                                                                                                                                                        X.W.,
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Qiang
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ID Q8WZ19
AC Q8B
AC Q8B
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Best Local
                                  Q8WZ19
Q8WZ19;
Q1-MAR-2002 (TIEMBLITEL 20, Created)
Q1-MAR-2002 (TIEMBLITEL 20, Last sequence up
Q1-JUN-2002 (TIEMBLITEL 21, Last annotation
Hypothetical 36.4 kDa protein.
Hypothetical 36.4 kDa protein.
Homo sapiens (Human).
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01-DEC-2001
01-DEC-2001
01-MAR-2002
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Mammalia; Eutheria;
NCBI_TaxID-9606;
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Homo sapiens (Human).
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 SGQPAAGRVMPGAARRARGMVVVTGREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRHYIPTDSEGRYFIDRDGTHFGDVLNFLRSGDLPPRERVRAVYK --- EAQYYAIGPLLE 234
                                                                                                                                                                                                                                                                                                                            DCQLALQQKRETLSPL
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                                                                                                                                                                                                                                                                                                                                                                                                                   GRVEVLTDAGGWVLIDRSGRHFGTILNYLRDGSVPLPESTRELGELLGEARYYLVQGLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEAPKPSGLEPGPAAYGLKPLTPNS--KYVKLNVGGSLHYTT-LRTL-TGQDTMLKAMFS 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGESVVSSAVPAAATRTTSF---KGTSPSSK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                        Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329 AA;
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                                                                                                                                                                                                                                                                                                                                                                          -QLENMQPL 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -YVKLNVGGALYYTTMQTL-TKQDTMLKAMFSGRMEVLTDSEGWILIDRCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BTB;
                 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TB; 1.
36371 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.5%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 204; DB 4;
Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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Pred. No. 8.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61092C2B0E81EA2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                             update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.5%;
Best Local Similarity 41.2%;
Matches 56; Conservative 1
                                             Matches
                                                                                          PROSITE;
SEQUENCE
                                                                                                    Pfam; PF02214; K_tetra; 1.
SMART; SM00225; BTB; 1.
PROSITE; PS50097; BTB; 1.
                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                      Q18986;
01-NOV-1996 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-2000) to the E
EMBL; ARL55757.1; -
EMBL; IPR0002131; BTB_POZ.
InterPro; IPR0003131; K_tetra.
Pfam; PF02214; K_tetra; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang
Wan D
                                                                                                                                                            investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z35639; CAA84696.1; -.
                                                                                                                                                                                                                                                                                                                                                          D2045.8 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                      Q18986
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Hypothetical protein.
SEQUENCE 329 AA; 36357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth.
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                      Submitted (AUG-1994)
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   NCHI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                  D2045.8
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SEQUENCE FROM
                                                                                                                                     InterPro; IPR000210; BTB_POZ.
InterPro; IPR003131; K_tetra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 LEPATPTATQAGHAL----PLLPQEFPEVVPLNIGGA-HFTTRLSTLRCYEDIMLAAMFS 177
                     123 LEPATPTATQAGHALPLLPQEFPEVVPLNIGGAHFTTRLSTLRCYEDTMLAAMFSGRHYI 182
                                                                                                                                                                                              Genome sequence of the nematode C.elegans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCQLALQQKRETLSPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----QLENMQPL 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H.
                                             64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human cDNA clones with function of inhibiting cancer cell
                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gu J
                                                                                          220 AA;
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao
.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BTB;
                                                                                                                                                                                                                                                                                                               Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36357 MW;
                                                                                          25651 MW;
                                                       11.2%;
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                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                        Score 200; DB 5;
Pred. No. 1.6e-07;
-IVKLDVGGKIFKTTIFTL-CKHDSMLKTMFCTDVPV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 204; DB 4;
Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                         D4E755FBBF7D3296 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17A8AC2DBE81EE78 CRC64;
                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     220
                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                          Rhabditida; Rhabditoidea;
                                                                                                                                                                                             A platform
                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 329
                                                                Length 220;
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                                             Indels
                                             48;
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                                           Gaps
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                                                                                                                                                                RA Adams N.D., Calniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Hilb P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Hilb P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Holt P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Holt P.W., Hoskins R.A., Galle R.F., RA Amanatides P. B.D., RA Brandon R.C., Rogers Y.H.C., Blazed R.G., Champe M., Pfelffer B.D., RA Brandon R.C., Rogers Y.H.C., Blazed R.G., Champe M., Pfelffer B.D., RA Brandon R.C., Rogers Y.H.C., Blazed R.G., Champe M., Pfelffer B.D., RA Brandon R.C., Rogers Y.H.C., Blazed R.G., Champe M., Pfelffer B.D., Ra Burtis R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Adopayani A., An H.-J., Andrews-Pfannboch C., Baldwin D., Borchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Blazed P., Baxendale J., Bryraktaroglu L., Beasley E.M., RA Bleeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Lordy R.G., Bayenport L.B., Davies P., RA Burtis K.C., Blayam D.A., Butler H., Cadleu E., Center A., Chandra I., Ra Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Fosler C., Brariera S., Fleischmann W., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Harris N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J., Ra Harris N.L., Harvey D., Kraft C., Kravitz S., Kennison J.A., Ketchum K.A., Ra Harris N.L., Matcheld M.V., Mcleod M.Y., Kelp D., Lai Z., Liang Y., Lin X., Jalai M., Kallysh F., Karft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Matcheld M.V., Mohary C., Morris J., Mosherson D.L., Ra Fleich J.M., Nathal R., Sanders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Sinpson M., Skupski M.P., Smith T., Ra Palazeolo M., Pithan G.N., Venter E., Wang A.H., Wang X., Wang X., Wang S., Yao Q.A., Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000
01-MAY-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9V9F4;
                          Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friss George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Trachaata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG10465
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                                                                                                              STRAIN-BERKELEY;
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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      Wan K.,
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Yu C.,
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Query Match
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Watches 62; Conserv
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SMART; SM00225; BTB; 1.
SEQUENCE 301 AA; 34048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymerase delta-interacting protein 1
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that interacts with the small subunit of DNA polymerase delta and proliferating cell nuclear antigen."; Proc. Natl. Acad. Sci. U.S.A. 98:11979-11984(2001).
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InterPro; IPR003131; K_tetra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000210; BTB_POZ.
InterPro; IPR003131; K_tetra.
Pfam; PF02214; K_tetra; 1.
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                                                                                                                178
                                                                                                                                                                                                                            123 LEPATPTATQAGHAL----PLLPQEFPEVVPLNIGGA-HFTTRLSTLRCYEDTMLAAMFS 177
235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                         16
                                                         72
                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H., Tan C.K., Downey K.M., So A.G.; tumor necrosis factor alpha - and interleukin 6-inducible protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLRFN-ERILFIKDVIGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGEKVROAFLGLMPYYKDHLERIVEIARLRAVQRKARFAKLKSLTPSWLMSVLIKMPPGV 302
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                                                                                                                                                                      GRLEVLTDAGSWYLIDRSGRHFGTILNYLRDGSVPLPESTKELGELLGEARYYLVQGLIE 131
                                                                                                            GRHYIPTDSEGRYFIDRDGTHFGDVLNFLRSGDLPPRERVRAVYK---EAQYYAIGPLLE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50097; BTB;
                                                                                                                                                                                                                                                                                                                                                                                                         329 AA;
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QLENMQPL 242
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                                                                                                                                                                                                                                                                                                                    10.8%; Score 193; DB 4; 37.5%; Pred. No. 8.9e-07;
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Pred. No. 4.7e-07;
2; Mismatches 76
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                                                                                                                                                                                                                                                                                                                                                                                                            D356490B48995187 CRC64;
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                                                                                                                                                                                                                                                                                            Mismatches
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01-MAR-2002
01-MAR-2002
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC019929; AAH19929.1; ...
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                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
NON_TER 1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical 36.2 kDa protein (Fragment).
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02214; K_tetra; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000210; BTB_POZ.
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                                                                                                                                                                                                                                                                    123 LEPATPTATQAGHAL-----PLLPQEFPEVVP------LNIGGAHFTTRLSTL
264 PVELP 268
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                             PVQLP 334
                                                         ELSSYQVDTFRANLFCTDSECLGALRARF -- GVASGDRAEGSPHFHLEWAPR--
                                                                                      RLRAVQRKARFAKLKSLTPSWLMSVLIKMPPGVTSWINAERRLYLETPIGPERQNNEKKS
                                                                                                                      ALLRAEADFYQIRPLLDALRELEASQGTPAPTA--ALLHADVDVSPRLVHFSARRGPHHY
                                                                                                                                                 AVYK-EAQYYAIGPLLEQLENMOPLKGEKVRQAFLGLMPYYKDHLERIVEIA-----
                                                                                                                                                                                 TRFPDSMLGAMFRAGTPMPPNLNSQGGGHYFIDRDGKAFRHILNFLRLGRLDLPRGYGET
                                                                                                                                                                                                           RCYEDTMLAAMFSGRHYIP----TDSEGRYFIDRDGTHFGDVLNFLRSG--DLPPRERVR 218
                                                                                                                                                                                                                                        LTASTQFCTHPGSSAFSFLSVSPVLPKISPPPVPSSPPSFGGPVTLNVGGTLYSTTLETL
                                                                                                                                                                                                                                                                                                                                                                                                        SM00225; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                           333 AA; 36219 MW;
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                                                                                                                                                                                                                                                                                                              10.8%; Score 192.5;
30.2%; Pred. No. 9.9
                                                                                                                                                                                                                                                                                                   28; Mismatches
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                                                                                                                                                                                                                                                                                                                                                             657EB138167D5F6B CRC64;
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